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OW protein - protein search, using sw model

Run on: July 15, 2004, 17:55:27 ; Search time 54 Seconds

(without alignments)  
2150.500 Million cell updates/sec

Title: US-09-980-350-2

Sequence: 1 MAPDLDPKSAQNSKPRLL.....LNGLPHCAGEIAVENIK 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29rand04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID      | Description         |
|------------|--------|-------------|--------|------------|---------------------|
| 1          | 2098   | 100.0       | 411    | 2 AAY34133 | Aay34133 Human pot  |
| 2          | 2098   | 100.0       | 411    | 2 AAY28496 | Aay28496 h-TREX1 p  |
| 3          | 2098   | 100.0       | 411    | 4 AAB50044 | Aab50044 Human TRE  |
| 4          | 2095   | 99.9        | 411    | 3 AAE10341 | Aae10341 Human TRE  |
| 5          | 2087   | 99.5        | 411    | 5 AAE16597 | Aae16597 Human TWI  |
| 6          | 2085   | 98.4        | 426    | 4 AAO7618  | AAO7618 Human pot   |
| 7          | 2061   | 98.2        | 426    | 4 AAO7622  | AAO7622 Human pot   |
| 8          | 2060   | 98.2        | 426    | 4 AAO7623  | AAO7623 Human pot   |
| 9          | 2057   | 98.0        | 426    | 4 AAO7625  | AAO7625 Human pot   |
| 10         | 2056   | 98.0        | 426    | 4 AAO7624  | AAO7624 Human pot   |
| 11         | 2044   | 97.4        | 411    | 3 AAE10342 | Aae10342 Murine TR  |
| 12         | 2038   | 97.1        | 411    | 2 AAY28497 | Aay28497 Mouse h-T  |
| 13         | 1833   | 87.4        | 370    | 2 AAY30648 | Aay30648 A mechani  |
| 14         | 1641.5 | 78.2        | 337    | 6 ABR41487 | Abri41487 Human DIT |
| 15         | 1242.5 | 59.2        | 538    | 5 AAB47930 | Aab47930 Human TRE  |
| 16         | 1242.5 | 59.2        | 538    | 5 AAE16596 | Aae16596 Human TWI  |
| 17         | 1242.5 | 59.2        | 538    | 5 AABP6933 | Abp6933 Human pol   |
| 18         | 1242.5 | 59.2        | 543    | 5 AAE21804 | Aae21804 Human TRE  |
| 19         | 1242.5 | 59.2        | 543    | 5 AAO81354 | AAO81354 Human hum  |
| 20         | 1242.5 | 59.2        | 543    | 5 AAU79472 | AAU79472 Human nov  |
| 21         | 1242.5 | 59.2        | 543    | 5 AAB83542 | Abb83542 Hypochala  |
| 22         | 1242.5 | 59.2        | 543    | 6 ADA05746 | Ada05746 Human NOV  |
| 23         | 1242.5 | 59.2        | 543    | 7 ADE08315 | Ade08315 Novel pro  |
| 24         | 1238.5 | 59.0        | 543    | 5 AAU79473 | AAU79473 Human nov  |
| 25         | 1215   | 57.9        | 724    | 5 AAO14193 | AAO14193 Human tra  |

|    |       |      |      |            |                    |
|----|-------|------|------|------------|--------------------|
| 26 | 803   | 38.3 | 392  | 6 ABU60891 | Abu60891 Human G p |
| 27 | 803   | 38.3 | 393  | 3 AAY94426 | Aay94426 Human h-T |
| 28 | 803   | 38.3 | 393  | 3 AAY94425 | Aay94425 Human h-T |
| 29 | 803   | 38.3 | 393  | 4 AAG67777 | Aag67777 Human mec |
| 30 | 803   | 38.3 | 419  | 5 AAG78406 | Aag78406 Arino aci |
| 31 | 803   | 38.3 | 419  | 5 AAE38597 | Aae38597 Human pot |
| 32 | 803   | 38.3 | 1314 | 7 AAU04571 | AAU04571 Human G-P |
| 33 | 803   | 38.3 | 1314 | 6 ABU60872 | Abu60872 Human G p |
| 34 | 776.5 | 37.0 | 398  | 2 AAY30647 | Aay30647 A mechani |
| 35 | 768.5 | 36.6 | 398  | 5 AAE16598 | Aae16598 Human TWI |
| 36 | 635.5 | 30.3 | 383  | 4 ABG02731 | ABG02731 Novel hum |
| 37 | 578.5 | 27.6 | 421  | 4 ABR12229 | ABR12229 Human K c |
| 38 | 549   | 26.2 | 155  | 4 AAM24148 | Aam24148 Human EST |
| 39 | 549   | 26.2 | 155  | 4 ADE09289 | Ade09289 Novel pro |
| 40 | 547   | 26.1 | 107  | 2 AAY28498 | Aay28498 Partial h |
| 41 | 513   | 24.5 | 295  | 5 AAE21164 | Aae21164 Human TRI |
| 42 | 502.5 | 24.0 | 294  | 5 AAU99892 | AAU99892 Human pot |
| 43 | 502.5 | 24.0 | 294  | 6 ABG72802 | ABG72802 Human 667 |
| 44 | 498.5 | 23.8 | 292  | 5 AAU99893 | AAU99893 Rat potas |
| 45 | 498.5 | 23.8 | 292  | 5 AAU99894 | AAU99894 Mouse pot |

## ALIGNMENTS

RESULT 1  
ID AAY34133 standard; protein; 411 AA.  
XX AAY34133;  
XX  
XX 30-NOV-1999 (first entry)  
XX  
XX Human potassium channel K-Hnov59.  
XX  
XX Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;  
XX  
XX cardiovascular disorder; CNS disorder; renal disorder.  
XX  
XX Homo sapiens.  
XX  
XX W09943696-A1.  
XX  
XX 02-SEP-1999.  
XX  
XX 22-FEB-1999; 99WO-US003826.  
XX  
XX 25-FEB-1998; 98US-0076687P.  
XX  
XX 07-AUG-1998; 98US-0095836P.  
XX  
XX 19-JAN-1999; 99US-0116448P.  
XX  
XX (AXYS-) AXYS PHARM INC.  
XX  
XX Miller AP, Curran ME, Hu P, Rutter M, Wang J;  
XX WPI; 1999-527591/44.  
XX N-PSDB; AA211915.  
XX  
XX New nucleic acids encoding mammalian K-Hnov potassium channel proteins,  
XX useful for the diagnosis and treatment of episodic ataxia with myokymia,  
XX cardiac arrhythmia, epilepsy and Bartter's syndrome.  
XX  
XX Claim 3; Page 104-105; 112pp; English.  
XX  
XX This sequence represents the human K-Hnov59 potassium channel. K-Hnov  
XX proteins have a high degree of homology to known potassium channels and  
XX may be alpha subunits, which form the functional channel, or accessory  
XX subunits that act to modulate the channel activity. K-Hnov59 is a 4  
XX transmembrane domain, 2 pore domain potassium channel. The gene is  
XX located on chromosome 19, determined via PCR chromosomal localisation  
XX using primers AA211939 and AA211940. K-Hnov cDNAs were isolated by  
XX extension of expressed sequence tags (ESTs) which were related but not  
XX identical to known human potassium channels. Potential polymorphisms  
XX detected as sequence variants between multiple independent clones.

CC Potassium channels have critical roles in various cell types and  
 CC biochemical pathways. Defective potassium channels are known to cause  
 CC four human diseases: episodic ataxia with myokymia; cardiac arrhythmia  
 CC (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium  
 CC channels are critical components of virtually all cells, it is likely  
 CC that abnormal potassium channels are also implicated in certain renal,  
 CC cardiovascular and central nervous system (CNS) disorders. Nucleotides  
 CC encoding K+Hov proteins may be used for identifying homologous or  
 CC related proteins and the DNA sequences encoding them. They may be used to  
 CC produce compositions that modulate the expression and function of the  
 CC K+Hov protein and in studying the biochemical pathways associated with  
 CC it. They may also be used for the recombinant production of K+Hov  
 CC protein in fermentation cultures. Additionally, such nucleotides may be  
 CC used in gene therapy protocols for the treatment of diseases associated  
 CC with abnormal potassium channels

CC Sequence 411 AA;

Query Match 100.0%; Score 2098; DB 2; Length 411;

Best Local Similarity 100.0%; Pred. No. 1.4e-208; Mismatches 0; Gaps 0;

Matches 411; Conservative 0; Indels 0; Gaps 0;

DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLAASRVESDTINWKKMKTGSTIFLVVLYLI 60  
 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLAASRVESDTINWKKMKTGSTIFLVVLYLI 60  
 QY 61 GATVFKALPHEISORTTIVIOKOTFISQHSQVNSTELDELIOQVAIINAGIIPLGNT 120  
 DB 61 GATVFKALPHEISORTTIVIOKOTFISQHSQVNSTELDELIOQVAIINAGIIPLGNT 120  
 QY 121 SNOISHMDLSSFFPAGVITITIGFQNSIPRTEGKIFCIYALGIPFGFLAGVGDQ 180  
 DB 121 SNOISHMDLSSFFPAGVITITIGFQNSIPRTEGKIFCIYALGIPFGFLAGVGDQ 180  
 QY 181 LGTIFPGKIAKVEDTPIKNNVSQTKIRIISTIIIFLFGCVLFAVPAIIFKHIEGWSALD 240  
 DB 181 LGTIFPGKIAKVEDTPIKNNVSQTKIRIISTIIIFLFGCVLFAVPAIIFKHIEGWSALD 240  
 QY 241 AIFVAVITLTITIGFGDYVAGSDIEYLDYKPVWFWIIVGLAYPAVLSMIGDMLRVIS 300  
 DB 241 AIFVAVITLTITIGFGDYVAGSDIEYLDYKPVWFWIIVGLAYPAVLSMIGDMLRVIS 300  
 QY 301 KKTKEVGEFRAHAAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNNQ 360  
 DB 301 KKTKEVGEFRAHAAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNNQ 360  
 QY 361 ELTPCRRITLSVNHLTSESDVLPPLKTBESIYINGLTPHCAGEIIVAVIENIK 411  
 DB 361 ELTPCRRITLSVNHLTSESDVLPPLKTBESIYINGLTPHCAGEIIVAVIENIK 411

RESULT 2

AA28496

ID AAY28496 standard; protein; 411 AA.

AC AAY28496;

DT 12-OCT-1999 (first entry)

DE h-TREK1 polypeptide.

KM h-TREK1; two pore potassium channel; inflammatory disease;

KM chromosome 1q32.

OS Homo sapiens.

PN WO9337762-A1.

PD 29-JUL-1999.

PF 02-DEC-1998; 98WO-EP007805.

PR 27-JAN-1998; 98EP-00300570.

PR 09-OCT-1998; 98GB-00022135.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA Meadows HT, Chapman CG;  
 PI WPI; 1999-469126/39.  
 DR N-PSDB; AA200039.  
 XX New two pore potassium channel used for, e.g. treatment of cancer,  
 PT pulmonary, cardiovascular and inflammatory diseases.  
 PS Claim 3; Page 24; 44pp: English.

XX This sequence is the h-TREK1 polypeptide, encoded by the h-TREK1  
 CC polynucleotide AA200039. h-TREK1 is a two pore potassium channel, and the  
 CC gene maps to human chromosome 1q32, between the markers DIS237 and  
 CC W15105. The polynucleotide sequence of h-TREK1 can be used to diagnose a  
 CC disease or susceptibility to a disease related to expression or activity  
 CC of h-TREK1 polypeptides. The methods of diagnosis may be used in the  
 CC treatment of diseases including cancer, pulmonary, cardiovascular, and  
 CC inflammatory diseases, pain, psychiatric disorders including depression  
 CC and schizophrenia, neurodegenerative diseases including Alzheimer's,  
 CC stroke, and head trauma and neurological disorders including migraine

SO Sequence 411 AA;

Query Match 100.0%; Score 2098; DB 2; Length 411;

Best Local Similarity 100.0%; Pred. No. 1.4e-208; Mismatches 0; Gaps 0;

Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLAASRVESDTINWKKMKTGSTIFLVVLYLI 60  
 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLAASRVESDTINWKKMKTGSTIFLVVLYLI 60  
 QY 61 GATVFKALPHEISORTTIVIOKOTFISQHSQVNSTELDELIOQVAIINAGIIPLGNT 120  
 DB 61 GATVFKALPHEISORTTIVIOKOTFISQHSQVNSTELDELIOQVAIINAGIIPLGNT 120  
 QY 121 SNOISHMDLSSFFPAGVITITIGFQNSIPRTEGKIFCIYALGIPFGFLAGVGDQ 180  
 DB 121 SNOISHMDLSSFFPAGVITITIGFQNSIPRTEGKIFCIYALGIPFGFLAGVGDQ 180  
 QY 181 LGTIFPGKIAKVEDTPIKNNVSQTKIRIISTIIIFLFGCVLFAVPAIIFKHIEGWSALD 240  
 DB 181 LGTIFPGKIAKVEDTPIKNNVSQTKIRIISTIIIFLFGCVLFAVPAIIFKHIEGWSALD 240  
 QY 241 AIFVAVITLTITIGFGDYVAGSDIEYLDYKPVWFWIIVGLAYPAVLSMIGDMLRVIS 300  
 DB 241 AIFVAVITLTITIGFGDYVAGSDIEYLDYKPVWFWIIVGLAYPAVLSMIGDMLRVIS 300  
 QY 301 KKTKEVGEFRAHAAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNNQ 360  
 DB 301 KKTKEVGEFRAHAAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNNQ 360  
 QY 361 ELTPCRRITLSVNHLTSESDVLPPLKTBESIYINGLTPHCAGEIIVAVIENIK 411  
 DB 361 ELTPCRRITLSVNHLTSESDVLPPLKTBESIYINGLTPHCAGEIIVAVIENIK 411

RESULT 3

AA50044

ID AAB50044 standard; protein; 411 AA.

AC AAB50044;

DT 19-MAR-2001 (first entry)

DE Human TREK.

KM Human; TREK; 2P domain potassium channel; resting membrane potential;  
 KM neuronal excitability; neurotransmitter release modulation; epilepsy;  
 KM neurological disorder; sleep-related disorder; cognitive dysfunction;

KM attention deficit disorder; addiction; anxiety; phobia;  
KM Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;  
KM erectile dysfunction; alopecia.  
XX  
XX Homo sapiens.  
XX MO200072863-A2.  
XX  
XX  
XX 07-DEC-2000.  
PD  
XX  
XX 01-JUN-2000; 2000MO-GB002107.  
PF  
XX  
XX 01-JUN-1999; 99GB-00012733.  
PR  
XX  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
PA  
XX  
XX Hervieu GJ, Meadows HJ, Randall AD;  
PI  
XX  
XX WPI; 2001-080422/09.  
DR  
XX  
XX N-PSDB; AAC90412.  
XX  
XX Use of human TREK1 polypeptide, polynucleotides encoding them and  
PT modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related  
PT disorders, addiction and dyskinesias including Parkinson's and  
PT Huntington's chorea.  
XX  
XX  
XX Claim 7; Page 29; 35pp; English.  
PS  
XX  
XX The present sequence is human TREK1 (h-TREK1). h-TREK1 is a member of the  
CC 2P domain potassium channel family of proteins which play a part in the  
CC control of resting membrane potential. Modulation of these channels will  
CC therefore affect neuronal excitability, thereby leading to a modulation  
CC of neurotransmitter release and activity of neuronal networks. Such  
CC modulation therefore may be useful for the treatment of certain  
CC neurological conditions such as epilepsy, sleep-related disorders,  
CC cognitive dysfunction, attention deficit disorder, addiction,  
CC anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy,  
CC incontinence, erectile dysfunction or alopecia  
XX  
XX  
XX Sequence 411 AA;  
SQ  
Query Match 100.0%; Score 2098; DB 4; Length 411;  
Best Local Similarity 100.0%; Pred. No. 1.4e-208;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTTFLVVVLYLI 60  
DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTTFLVVVLYLI 60  
QY 61 GATVFKALBQPHESORTTIVIQKOTFISQHSQNSVTELDLQOIVAAINAGIIPLGNT 120  
DB 61 GATVFKALBQPHESORTTIVIQKOTFISQHSQNSVTELDLQOIVAAINAGIIPLGNT 120  
QY 121 SNOISHMDLGSFFPAGVITTTIGFQNSIPRTGEGKFCITTYALLGIPLFGLLAGVGDQ 180  
DB 121 SNOISHMDLGSFFPAGVITTTIGFQNSIPRTGEGKFCITTYALLGIPLFGLLAGVGDQ 180  
QY 181 LGTIFGKGIKIAVEDTFIKMNSQTKIRIISTITFIIFGCVLFVALPAIIFKHIEGMSALD 240  
DB 181 LGTIFGKGIKIAVEDTFIKMNSQTKIRIISTITFIIFGCVLFVALPAIIFKHIEGMSALD 240  
QY 241 AIFEVVITLTITIGFGDVVAGGSDIEYDFKPVVWFMIIVGLAYFAAVLSMIGDMLRVIS 300  
DB 241 AIFEVVITLTITIGFGDVVAGGSDIEYDFKPVVWFMIIVGLAYFAAVLSMIGDMLRVIS 300  
QY 301 KKTKEVEGEFRRAHAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNHNQ 360  
DB 301 KKTKEVEGEFRRAHAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNHNQ 360  
QY 361 ELTPCRRITLSVNHLSERDVLPLLKTESITLNGLPHQAGEIAVYENIK 411  
DB 361 ELTPCRRITLSVNHLSERDVLPLLKTESITLNGLPHQAGEIAVYENIK 411

RESULT 4  
AAE10341  
ID AAE10341 standard; protein, 411 AA.  
XX  
XX  
XX AAE10341;  
AC  
XX  
XX 10-DEC-2001 (first entry)  
DT  
XX  
XX Human TREK-1 potassium channel protein.  
DE  
XX  
XX Human TREK-1 potassium channel protein; TREK-1; anaesthetic; analgesia;  
KW amnesia.  
KW  
XX  
XX Homo sapiens.  
OS  
XX  
XX MO200047738-A2.  
PN  
XX  
XX 17-AUG-2000.  
PD  
XX  
XX 11-FEB-2000; 2000MO-IB000226.  
PF  
XX  
XX 12-FEB-1999; 99US-0119727P.  
PR 11-FEB-2000; 2000US-00503089.  
XX  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
XX  
XX  
XX Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;  
PI  
XX  
XX WPI; 2000-549146/50.  
DR  
XX  
XX N-PSDB; AAD17496.  
XX  
XX Novel nucleic acid encoding a TREK-1 potassium channel protein for  
PT transfecting cells to be used to identify compounds with anesthetic  
PT properties.  
XX  
XX  
XX Claim 3; Page 28; 35pp; English.  
PS  
XX  
XX The invention relates to human and mouse TREK-1 potassium channel  
CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is  
CC useful for transfecting cells to induce expression of the TREK-1  
CC potassium channel protein. These cells are then used in assays to  
CC identify compounds which have anaesthetic properties, producing a safe,  
CC reversible state of unconsciousness with concurrent amnesia and analgesia  
CC in a mammal upon inhalation. The present sequence is human TREK-1  
CC potassium channel protein  
XX  
XX  
XX Sequence 411 AA;  
SQ  
Query Match 99.9%; Score 2095; DB 3; Length 411;  
Best Local Similarity 99.8%; Pred. No. 2.9e-208;  
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTTFLVVVLYLI 60  
DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTTFLVVVLYLI 60  
QY 61 GATVFKALBQPHESORTTIVIQKOTFISQHSQNSVTELDLQOIVAAINAGIIPLGNT 120  
DB 61 GATVFKALBQPHESORTTIVIQKOTFISQHSQNSVTELDLQOIVAAINAGIIPLGNT 120  
QY 121 SNOISHMDLGSFFPAGVITTTIGFQNSIPRTGEGKFCITTYALLGIPLFGLLAGVGDQ 180  
DB 121 SNOISHMDLGSFFPAGVITTTIGFQNSIPRTGEGKFCITTYALLGIPLFGLLAGVGDQ 180  
QY 181 LGTIFGKGIKIAVEDTFIKMNSQTKIRIISTITFIIFGCVLFVALPAIIFKHIEGMSALD 240  
DB 181 LGTIFGKGIKIAVEDTFIKMNSQTKIRIISTITFIIFGCVLFVALPAIIFKHIEGMSALD 240  
QY 241 AIFEVVITLTITIGFGDVVAGGSDIEYDFKPVVWFMIIVGLAYFAAVLSMIGDMLRVIS 300  
DB 241 AIFEVVITLTITIGFGDVVAGGSDIEYDFKPVVWFMIIVGLAYFAAVLSMIGDMLRVIS 300

QY 301 KKTKEVGEFRAHAAMWTAVTAEFKETRRLSVEIYDKFORATSIKRKLAEIAGNHQ 360  
 DB 301 KKTKEVGEFRAHAAMWTAVTAEFKETRRLSVEIYDKFORATSIKRKLAEIAGNHQ 360  
 QY 361 ELTPCRRITLSVNLHJTSERDVLPLLTKESTIYNGLTPLHCAEIAIENIK 411  
 DB 361 ELTPCRRITLSVNLHJTSERDVLPLLTKESTIYNGLTPLHCAEIAIENIK 411

RESULT 5  
 ID AAE16597 standard; protein; 411 AA.  
 AC AAE16597;

DT 18-APR-2002 (first entry)  
 DE Human TWIK-Related K<sup>+</sup> Channel-1 (TREK-1) protein.  
 XX Human; TWIK-Related K<sup>+</sup> Channel-1; TREK-1; anaesthetic; screening.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH 47..65  
 FT /note="M1 membrane spanning segment"  
 FT 127..150  
 FT Domain /note="P1 pore domain"  
 FT 158..178  
 FT Region /note="M2 membrane spanning segment"  
 FT 209..230  
 FT Region /note="M3 membrane spanning segment"  
 FT 236..259  
 FT Domain /note="P2 pore domain"  
 FT 274..293  
 FT Region /note="M4 membrane spanning segment"

W0200200715-A2.

03-JAN-2002.

27-JUN-2001; 2001WO-IB001436.

27-JUN-2000; 2000US-0214559P.

27-JUN-2001; 2001US-00892360.

(CNRS ) CNRS CENT NAT RECH SCI.

Lazdunski M, Lesage F, Romey G;

WPI; 2002-139903/18.

New mammalian K<sup>+</sup> channel protein with two pore domains, for screening various compounds, particularly for identifying biologically active compounds with anesthetic properties.

Disclosure; Fig 1A; 50pp; English.

The invention relates to a mammalian K<sup>+</sup> channel protein with two pore domains, called TREK2 (TWIK-Related K<sup>+</sup> Channel). The protein produces currents whose current-voltage relationship is slightly inwardly rectifying in high symmetrical K<sup>+</sup> conditions. TREK2 is a member of the fatty acid-activated and mechanosensitive K<sup>+</sup> channel family. TREK-2 gene located on chromosome 14q31 is abundantly expressed in kidney, pancreas and moderately in testis, brain, colon and small intestine. The mammalian K<sup>+</sup> channel protein is useful in methods for screening various compounds. In particular, the protein is useful in methods for identifying biologically active compounds with anesthetic properties. The present sequence is TREK-1 protein used in the invention

Sequence 411 AA;

Query Match 99.5%; Score 2087; DB 5; Length 411;

Best Local Similarity 99.5%; Pred. No. 2e-207; Indels 0; Gaps 0;  
 Matches 409; Conservative 1; Mismatches 1;  
 QY 1 MAAPDLDPKSAQONKSPRLSFTKPTVLASRVESDTTINVMKKTSTIPLVVVLYII 60  
 DB 1 MAAPDLDPKSAQONKSPRLSFTKPTVLASRVESDTTINVMKKTSTIPLVVVLYII 60  
 QY 61 GATVPKALBOPHEISQRTTIVIOKOTFISQSCVNSTEIDELIOQVAAINAGIPLGNT 120  
 DB 61 GATVPKALBOPHEISQRTTIVIOKOTFISQSCVNSTEIDELIOQVAAINAGIPLGNT 120  
 QY 121 SNOISHWDGSSFPFGATVTTTIGFNGISPRTEGKIFCIYALGIPFGFLAGVQ 180  
 DB 121 SNOISHWDGSSFPFGATVTTTIGFNGISPRTEGKIFCIYALGIPFGFLAGVQ 180  
 QY 181 LGTIFGKIAKVEDTIFKMWVSOQTKIRIISTITFIIFGCVLPVALPAIIFKHIEGMSAD 240  
 DB 181 LGTIFGKIAKVEDTIFKMWVSOQTKIRIISTITFIIFGCVLPVALPAIIFKHIEGMSAD 240  
 QY 241 AIYFVYVITLTITIGFGYVAGGSDIEYLDPKPVVMFIIVGLAYFAAVLSMIGDMLRVIS 300  
 DB 241 AIYFVYVITLTITIGFGYVAGGSDIEYLDPKPVVMFIIVGLAYFAAVLSMIGDMLRVIS 300  
 QY 301 KKTKEVGEFRAHAAMWTAVTAEFKETRRLSVEIYDKFORATSIKRKLAEIAGNHQ 360  
 DB 301 KKTKEVGEFRAHAAMWTAVTAEFKETRRLSVEIYDKFORATSIKRKLAEIAGNHQ 360  
 QY 361 ELTPCRRITLSVNLHJTSERDVLPLLTKESTIYNGLTPLHCAEIAIENIK 411  
 DB 361 ELTPCRRITLSVNLHJTSERDVLPLLTKESTIYNGLTPLHCAEIAIENIK 411

RESULT 6

AAU07618 standard; protein; 426 AA.

AAU07618;

21-NOV-2001 (first entry)

Human potassium ion channel TPCK1 protein.

Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihelminthic; nematode;

Insect; TPCK1; human.

Homo sapiens.

W0200161006-A2.

23-AUG-2001.

14-FEB-2001; 2001WO-US004680.

15-FEB-2000; 2000US-00503849.

(BADI ) BASF CORP.

Pausch ME;

WPI; 2001-536570/59.

N-PSDB; AAS12169.

New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions.

Example 15; Page 45; 131pp; English.

The invention relates to a mutant potassium ion channel protein, having a four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their

CC corresponding polynucleotide sequences can therefore be used to improve  
 CC inward potassium flux into cells under acidic conditions by modulating  
 CC the membrane potential using therapeutic agents. The sequences may be  
 CC used to develop agonists and antagonists of potassium channel proteins in  
 CC order to control pests such as nematodes and insects. This sequence  
 CC represents a human transmembrane potassium ion channel protein, TPCK1  
 XX

XX Sequence 426 AA;

Query Match 98.4%; Score 2065; DB 4; Length 426;  
 Best Local Similarity 98.8%; Pred. No. 4e-205;  
 Matches 406; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFTKPTVLASRVESDTTINVMKKTIVSTIFLVVLYLI 60  
 DB 16 VAAPDLDPKSAQNSKPRLSFTKPTVLASRVESDTTINVMKKTIVSTIFLVVLYLI 75  
 QY 61 GATVFKALDQPHISQRTTIVIOKOTFISQSCVNSTELDELIOQIVAAINAGIIPLGNT 120  
 DB 76 GATVFKALDQPHISQRTTIVIOKOTFISQSCVNSTELDELIOQIVAAINAGIIPLGNT 135  
 QY 121 SNOISHMDLGSSFFPAGTIVITTFGNISPRTEGKIFCIITVALGIPFGFLAGVGQ 180  
 DB 136 SNOISHMDLGSSFFPAGTIVITTFGNISPRTEGKIFCIITVALGIPFGFLAGVGQ 195  
 QY 181 LGTIFGKGIKAVEDTTFIKMNSQTKRIISTITIFILGCVLPAALPFKHIEGMSALD 240  
 DB 196 LGTIFGKGIKAVEDTTFIKMNSQTKRIISTITIFILGCVLPAALPFKHIEGMSALD 255  
 QY 241 AIFEVVITLTITIGFDVYAGSDIEYDFYKPVWFMILVGLAFPAVLMSIGMLRVIS 300  
 DB 256 AIFEVVITLTITIGFDVYAGSDIEYDFYKPVWFMILVGLAFPAVLMSIGMLRVIS 315  
 QY 301 KKTKEVGEFPAHAEMTANTVTAFFKETRRLSVEIYDKFORATSIKRLSAGELAGNHQ 360  
 DB 316 KKTKEVGEFPAHAEMTANTVTAFFKETRRLSVEIYDKFORATSIKRLSAGELAGNHQ 375  
 QY 361 ELTPCRTLSTVNLTSERDVPPLKTESIYNLGLTPHCAGEEIAVENIK 411  
 DB 376 ELTPCRTLSTVNLTSERDVPPLKTESIYNLGLTPHCAGEEIAVENIK 426

RESULT 7

AAU07622 ID AAU07622 standard; protein; 426 AA.

XX AC AAU07622;

XX DT 21-NOV-2001 (first entry)

XX DE Human potassium ion channel TPCK1 mutant protein #1.

XX KW Transmembrane potassium ion channel protein; inward potassium flux;

XX KM pest control; membrane potential; pesticide; antihelminthic; nematode;

XX KM insect; TPCK1; human; mutant; mutein.

XX OS Homo sapiens.

XX FT Key Location/Qualifiers

XX FT Misc-difference 256 /note= "wild-type Ala replaced by Thr"

XX FT WO200161006-A2.

XX PD 23-AUG-2001.

XX PF 14-FEB-2001; 2001MO-US004680.

XX PR 15-FEB-2000; 2000US-00503849.

XX PA (BADI ) BASF CORP.

XX PA Pausch WH;

XX WP1; 2001-536570/59.  
 XX DR N-PSDB; AAS12181.

XX PT New polypeptide, a mutant potassium ion channel protein for improving  
 XX inward potassium flux under acidic conditions.

XX PS Claim 37; Page 113-115; 131pp; English.

XX The invention relates to a mutant potassium ion channel protein, having  
 XX four membrane spanning domains and two pore forming domains, comprising a  
 XX mutation at the second pore forming domain. The expression of the mutant  
 XX protein in a cell confers improved inward potassium flux and the ability  
 XX to grow in the presence of potassium. Mutant proteins and their  
 XX corresponding polynucleotide sequences can therefore be used to improve  
 XX inward potassium flux into cells under acidic conditions by modulating  
 XX the membrane potential using therapeutic agents. The sequences may be  
 XX used to develop agonists and antagonists of potassium channel proteins in  
 XX order to control pests such as nematodes and insects. This sequence  
 XX represents a human transmembrane potassium ion channel TPCK1 mutant  
 XX protein

XX Sequence 426 AA;

Query Match 98.2%; Score 2061; DB 4; Length 426;  
 Best Local Similarity 98.5%; Pred. No. 1e-204;  
 Matches 405; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFTKPTVLASRVESDTTINVMKKTIVSTIFLVVLYLI 60  
 DB 16 VAAPDLDPKSAQNSKPRLSFTKPTVLASRVESDTTINVMKKTIVSTIFLVVLYLI 75  
 QY 61 GATVFKALDQPHISQRTTIVIOKOTFISQSCVNSTELDELIOQIVAAINAGIIPLGNT 120  
 DB 76 GATVFKALDQPHISQRTTIVIOKOTFISQSCVNSTELDELIOQIVAAINAGIIPLGNT 135  
 QY 121 SNOISHMDLGSSFFPAGTIVITTFGNISPRTEGKIFCIITVALGIPFGFLAGVGQ 180  
 DB 136 SNOISHMDLGSSFFPAGTIVITTFGNISPRTEGKIFCIITVALGIPFGFLAGVGQ 195  
 QY 181 LGTIFGKGIKAVEDTTFIKMNSQTKRIISTITIFILGCVLPAALPFKHIEGMSALD 240  
 DB 196 LGTIFGKGIKAVEDTTFIKMNSQTKRIISTITIFILGCVLPAALPFKHIEGMSALD 255  
 QY 241 AIFEVVITLTITIGFDVYAGSDIEYDFYKPVWFMILVGLAFPAVLMSIGMLRVIS 300  
 DB 256 TIFEVVITLTITIGFDVYAGSDIEYDFYKPVWFMILVGLAFPAVLMSIGMLRVIS 315  
 QY 301 KKTKEVGEFPAHAEMTANTVTAFFKETRRLSVEIYDKFORATSIKRLSAGELAGNHQ 360  
 DB 316 KKTKEVGEFPAHAEMTANTVTAFFKETRRLSVEIYDKFORATSIKRLSAGELAGNHQ 375  
 QY 361 ELTPCRTLSTVNLTSERDVPPLKTESIYNLGLTPHCAGEEIAVENIK 411  
 DB 376 ELTPCRTLSTVNLTSERDVPPLKTESIYNLGLTPHCAGEEIAVENIK 426

RESULT 8

AAU07623 ID AAU07623 standard; protein; 426 AA.

XX AC AAU07623;

XX DT 21-NOV-2001 (first entry)

XX DE Human potassium ion channel TPCK1 mutant protein #2.

XX KW Transmembrane potassium ion channel protein; inward potassium flux;

XX KM pest control; membrane potential; pesticide; antihelminthic; nematode;

XX KM insect; TPCK1; human; mutant; mutein.

XX OS Homo sapiens.

Key Location/Qualifiers  
 Misc-difference 272  
 /note= "Wild-type Tyr replaced by His"

XX MO200161006-A2.

XX 23-AUG-2001.

XX 14-FEB-2001; 2001WO-US004680.

XX 15-FEB-2000; 2000US-00503849.

XX (BAD1 ) BASF CORP.

XX Pausch MH;

XX WPI; 2001-536570/59.

XX N-PSDB; AAS12182.

XX New polypeptide, a mutant potassium ion channel protein for improving

XX inward potassium flux under acidic conditions.

XX Claim 37; Page 115-117; 131pp; English.

XX The invention relates to a mutant potassium ion channel protein, having  
 CC four membrane spanning domains and two pore forming domains, comprising a  
 CC mutation at the second pore forming domain. The expression of the mutant  
 CC protein in a cell confers improved inward potassium flux and the ability  
 CC to grow in the presence of potassium. Mutant proteins and their  
 CC corresponding polynucleotide sequences can therefore be used to improve  
 CC inward potassium flux into cells under acidic conditions by modulating  
 CC the membrane potential using therapeutic agents. The sequences may be  
 CC used to develop agonists and antagonists of potassium channel proteins in  
 CC order to control pests such as nematodes and insects. This sequence  
 CC represents a human transmembrane potassium ion channel TPKC1 mutant  
 CC protein

XX Sequence 426 AA;

XX Query Match 98.2%; Score 2060; DB 4; Length 426;

XX Best Local Similarity 98.5%; Pred. No. 1.3e-204;

XX Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAAPDLIDPKSAANQSKPRLSFTKPTVLASRVESDTTINWKMKTGSTIFLVVLYLI 60

DB 16 VAAPDLIDPKSAANQSKPRLSFTKPTVLASRVESDTTINWKMKTGSTIFLVVLYLI 75

QY 61 GATVFALQPHISQRTTIVQKQTFISQSCVNSTEDELIOQIVAAINAGIIPLGNT 120

DB 76 GATVFALQPHISQRTTIVQKQTFISQSCVNSTEDELIOQIVAAINAGIIPLGNT 135

QY 121 SNOISHWDLGSSFFFGAGTIVITIGFNGISPRTEGGKIFCIYALGIFLPGFLAGVGQ 180

DB 136 SNOISHWDLGSSFFFGAGTIVITIGFNGISPRTEGGKIFCIYALGIFLPGFLAGVGQ 195

QY 181 LGTIFGKGIAXVEDFTIKMNVQTKIRIISTIFILFGCVLFPALPFIHIBGWSALD 240

DB 196 LGTIFGKGIAXVEDFTIKMNVQTKIRIISTIFILFGCVLFPALPFIHIBGWSALD 255

QY 241 AIFVAVITLTIGFGDYVAGSDIEYLDPKYKPVWFILVGLAYFAALVSMIGDLRYIS 300

DB 256 AIFVAVITLTIGFGDYVAGSDIEYLDPKYKPVWFILVGLAYFAALVSMIGDLRYIS 315

QY 301 KKTKEVGFERRAAAEWMTANVTAEFKETRRRLSVEIYDKFORATSIKKKLSAELAGNNO 360

DB 316 KKTKEVGFERRAAAEWMTANVTAEFKETRRRLSVEIYDKFORATSIKKKLSAELAGNNO 375

QY 361 ELTPCARTLSVNHLSERDVPPLLKTBSIYNGLTPLHCAGEIAVIEINIK 411

DB 376 ELTPCARTLSVNHLSERDVPPLLKTBSIYNGLTPLHCAGEIAVIEINIK 426

RESULT 9

AAU07625  
 ID AAU07625 standard; protein; 426 AA.

XX AC AAU07625;

XX DT 21-NOV-2001 (first entry)

XX DE Human potassium ion channel TPKC1 mutant protein #4.

XX KW Transmembrane potassium ion channel protein; inward potassium flux;

XX KW pest control; membrane potential; pesticide; antihelminthic; nematode;

XX KW insect; TPKC1; human; mutant; mutein.

XX OS Homo sapiens.

XX FT Key Location/Qualifiers

XX FT Misc-difference 270

XX FT /note= "Wild-type Gly replaced by Arg"

XX MO200161006-A2.

XX 23-AUG-2001.

XX 14-FEB-2001; 2001WO-US004680.

XX 15-FEB-2000; 2000US-00503849.

XX (BAD1 ) BASF CORP.

XX Pausch MH;

XX WPI; 2001-536570/59.

XX N-PSDB; AAS12184.

XX New polypeptide, a mutant potassium ion channel protein for improving

XX inward potassium flux under acidic conditions.

XX Claim 37; Page 119-120; 131pp; English.

XX The invention relates to a mutant potassium ion channel protein, having  
 CC four membrane spanning domains and two pore forming domains, comprising a  
 CC mutation at the second pore forming domain. The expression of the mutant  
 CC protein in a cell confers improved inward potassium flux and the ability  
 CC to grow in the presence of potassium. Mutant proteins and their  
 CC corresponding polynucleotide sequences can therefore be used to improve  
 CC inward potassium flux into cells under acidic conditions by modulating  
 CC the membrane potential using therapeutic agents. The sequences may be  
 CC used to develop agonists and antagonists of potassium channel proteins in  
 CC order to control pests such as nematodes and insects. This sequence  
 CC represents a human transmembrane potassium ion channel TPKC1 mutant  
 CC protein

XX Sequence 426 AA;

XX Query Match 98.0%; Score 2057; DB 4; Length 426;

XX Best Local Similarity 98.5%; Pred. No. 2.7e-204;

XX Matches 405; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLIDPKSAANQSKPRLSFTKPTVLASRVESDTTINWKMKTGSTIFLVVLYLI 60

DB 16 VAAPDLIDPKSAANQSKPRLSFTKPTVLASRVESDTTINWKMKTGSTIFLVVLYLI 75

QY 61 GATVFALQPHISQRTTIVQKQTFISQSCVNSTEDELIOQIVAAINAGIIPLGNT 120

DB 76 GATVFALQPHISQRTTIVQKQTFISQSCVNSTEDELIOQIVAAINAGIIPLGNT 135

QY 121 SNOISHWDLGSSFFFGAGTIVITIGFNGISPRTEGGKIFCIYALGIFLPGFLAGVGQ 180

DB 136 SNOISHWDLGSSFFFGAGTIVITIGFNGISPRTEGGKIFCIYALGIFLPGFLAGVGQ 195

QY 181 LGTIFGKGIAXVEDFTIKMNVQTKIRIISTIFILFGCVLFPALPFIHIBGWSALD 240

DB 196 LGTIFGKGIAXVEDFTIKMNVQTKIRIISTIFILFGCVLFPALPFIHIBGWSALD 255

QY 241 AIYFVITLTITIGFDYVAGSDIEYDFKPVWFMLVGLAYFAVLISMIGDLRVIS 300  
 DB 256 AIYFVITLTITIGFRYVAGSDIEYDFKPVWFMLVGLAYFAVLISMIGDLRVIS 315  
 QY 301 KKTKEVEGFRRAHAEMTANVTAEFKETRRRLSVEIYDKFQATSIKRLSAELAGNHQ 360  
 DB 316 KKTKEVEGFRRAHAEMTANVTAEFKETRRRLSVEIYDKFQATSIKRLSAELAGNHQ 375  
 QY 361 ELTPCRRTLSVNHLSERDVLPLPKTESIYINGLTPHCAGEBIAVENIK 411  
 DB 376 ELTPCRRTLSVNHLSERDVLPLPKTESIYINGLTPHCAGEBIAVENIK 426  
 RESULT 10  
 AAU07624  
 ID AAU07624 standard; protein; 426 AA.  
 AC AAU07624;  
 DT 21-NOV-2001 (first entry)  
 XX Human potassium ion channel TPKC1 mutant protein #3.  
 DE Transmembrane potassium ion channel protein; inward potassium flux;  
 KM pest control; membrane potential; pesticide; antihelminthic; nematode;  
 KW insect; TPKC1; human; mutant; mutain.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 272 /note= "Wild-type Tyr replaced by His"  
 FT Misc-difference 274 /note= "Wild-type Ala replace by Val"  
 FT  
 XX MO200161006-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 14-FEB-2001; 2001WO-US004680.  
 XX  
 PR 15-FEB-2000; 2000US-00503849.  
 XX  
 PA (BAD1 ) BASP CORP.  
 PI Pausch MH;  
 PS  
 DR WPI; 2001-536570/59.  
 DR N-PSDB; AAS12183.  
 XX  
 PT New polypeptide, a mutant potassium ion channel protein for improving  
 XX inward potassium flux under acidic conditions.  
 PS Claim 37; Page 117-119; 13pp; English.  
 XX  
 CC The invention relates to a mutant potassium ion channel protein, having  
 CC four membrane spanning domains and two pore forming domains, comprising a  
 CC mutation at the second pore forming domain. The expression of the mutant  
 CC protein in a cell confers improved inward potassium flux and the ability  
 CC to grow in the presence of potassium. Mutant proteins and their  
 CC corresponding polynucleotide sequences can therefore be used to improve  
 CC inward potassium flux into cells under acidic conditions by modulating  
 CC the membrane potential using therapeutic agents. The sequences may be  
 CC used to develop agonists and antagonists of potassium channel proteins in  
 CC order to control pests such as nematodes and insects. This sequence  
 CC represents a human transmembrane potassium ion channel TPKC1 mutant  
 CC protein  
 XX  
 SQ Sequence 426 AA;  
 XX  
 Query Match 98.0%; Score 2056; DB 4; Length 426;  
 Best Local Similarity 98.3%; Pred. No. 3.4e-204;

Matches 404; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MAAPDLDPKSAQNSKRLSFSTKPTVLASRYESDPTINMMKTVSTIFLVVLYLLI 60  
 DB 16 VAAPDLDPKSAQNSKRLSFSTKPTVLASRYESDPTINMMKTVSTIFLVVLYLLI 75  
 QY 61 GAIVFKALEQPHHSISQRTTIVIOKQFIQSCHSCVNSTELDELQQIYVAANAAGIIPLGNT 120  
 DB 76 GAIVFKALEQPHHSISQRTTIVIOKQFIQSCHSCVNSTELDELQQIYVAANAAGIIPLGNT 135  
 QY 121 SNOISHMDLSSPFPAFTVITTTIGFNIISPTSGKIFCIYVALLGIFGFLLAGYDQ 180  
 DB 136 SNOISHMDLSSPFPAFTVITTTIGFNIISPTSGKIFCIYVALLGIFGFLLAGYDQ 195  
 QY 181 LGTIFGKGIKVEDTFIKMNVISQTKRIISTIIIFILGCVLPVALPAIIFKHIEGMSALD 240  
 DB 196 LGTIFGKGIKVEDTFIKMNVISQTKRIISTIIIFILGCVLPVALPAIIFKHIEGMSALD 255  
 QY 241 AIYFVITLTITIGFDYVAGSDIEYDFKPVWFMLVGLAYFAVLISMIGDLRVIS 300  
 DB 256 AIYFVITLTITIGFDYVAGSDIEYDFKPVWFMLVGLAYFAVLISMIGDLRVIS 315  
 QY 301 KKTKEVEGFRRAHAEMTANVTAEFKETRRRLSVEIYDKFQATSIKRLSAELAGNHQ 360  
 DB 316 KKTKEVEGFRRAHAEMTANVTAEFKETRRRLSVEIYDKFQATSIKRLSAELAGNHQ 375  
 QY 361 ELTPCRRTLSVNHLSERDVLPLPKTESIYINGLTPHCAGEBIAVENIK 411  
 DB 376 ELTPCRRTLSVNHLSERDVLPLPKTESIYINGLTPHCAGEBIAVENIK 426  
 RESULT 11  
 AAEI0342  
 ID AAEI0342 standard; protein; 411 AA.  
 AC AAEI0342;  
 DT 10-DEC-2001 (first entry)  
 XX  
 DE Murine TREK-1 potassium channel protein.  
 XX  
 KM Murine; potassium channel protein; TREK-1; anaesthetic; analgesia;  
 KW amnesia.  
 OS Mus musculus.  
 XX  
 PN WO200047738-A2.  
 PD 17-AUG-2000.  
 XX  
 PF 11-FEB-2000; 2000WO-IB000226.  
 XX  
 PR 12-FEB-1999; 99US-0119727P.  
 PR 11-FEB-2000; 2000US-00503089.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PI Lazdunski M, Honore F, Lesage F, Romey G, Patel AJ;  
 PS WPI; 2000-549146/50.  
 DR N-PSDB; AAD17497.  
 XX  
 PT Novel nucleic acid encoding a TREK-1 potassium channel protein for  
 XX transfecting cells to be used to identify compounds with anesthetic  
 XX properties.  
 PS Claim 9; Page 32-33; 39pp; English.  
 XX  
 CC The invention relates to human and mouse TREK-1 potassium channel  
 CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is  
 CC useful for transfecting cells to induce expression of the TREK-1  
 CC potassium channel protein. These cells are then used in assays to  
 CC identify compounds which have anaesthetic properties, producing a safe,

CC reversible state of unconsciousness with concurrent amnesia and analgesia  
CC in a mammal upon inhalation. The present sequence is murine TREK-1  
CC potassium channel protein  
XX

SO Sequence 411 AA;

Query Match 97.4%; Score 2044; DB 3; Length 411;  
Best Local Similarity 96.4%; Pred. No. 5.7e-203;  
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTNMWMKTVSTIFLVVLYLII 60  
DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTNMWMKTVSTIFLVVLYLII 60  
QY 61 GATVFKALBOPHISQRTTIVIOKQTFISQHSQVNSTEDELIOQIVAAINNGIPLGNT 120  
DB 61 GAATVFKALBOPHISQRTTIVIOKQTFISQHSQVNSTEDELIOQIVAAINNGIPLGNS 120  
QY 121 SNOISHMDLGSFFFGVITTTGFGNISPRTEGGKIFCIYALLGIPFGFLAGVGDQ 180  
DB 121 SNOISHMDLGSFFFGVITTTGFGNISPRTEGGKIFCIYALLGIPFGFLAGVGDQ 180  
QY 181 LGTIFGKGIKAVEDTIFKNNVSQTKRIISTIFILFGCVLFVALPAVIFKHEGMSALD 240  
DB 181 LGTIFGKGIKAVEDTIFKNNVSQTKRIISTIFILFGCVLFVALPAVIFKHEGMSALD 240  
QY 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVWFWIIVGLAAYFAVLSMTGDLRVIS 300  
DB 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVWFWIIVGLAAYFAVLSMTGDLRVIS 300  
QY 301 KKTKEVGFPRAAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNHNQ 360  
DB 301 KKTKEVGFPRAAEMTANVTAEFKETRRRLSVEIYDKFORATSIVKRLSALAGNHNQ 360  
QY 361 ELTPCRRITLSVNHLSERDVLPLLKTESIYNGLTPHCAGEIAVNIENIK 411  
DB 361 ELTPCRRITLSVNHLSERDVLPLLKTESIYNGLTPHCAGEIAVNIENIK 411

RESULT 12

ID AAY28497 standard; protein; 411 AA.

XX AAY28497;  
AC AAY28497;  
XX  
DT 12-OCT-1999 (first entry)  
XX  
DE Mouse h-TREK1 polypeptide.  
XX  
KW h-TREK1, two pore potassium channel; inflammatory disease;  
KW chromosome 1q32.  
XX  
OS Mus. musculus.  
XX  
PN WO937762-A1.  
XX  
PD 29-JUL-1999.  
XX  
PF 02-DEC-1998; 98WO-EP007805.  
XX  
PR 27-JAN-1998; 98EP-00300570.  
PR 09-OCT-1998; 98GB-00022135.  
XX  
PA (SMK) SMITHKLINE BEECHAM PLC.  
XX  
PI Meadows HJ, Chapman CG;  
XX  
DR WPI; 1999-469126/39.  
XX  
N-PSDB; AAC00040.  
XX  
PT New two pore potassium channel used for, e.g. treatment of cancer,  
XX pulmonary, cardiovascular and inflammatory diseases.

PS Claim 3; Page 26; 44pp; English.

XX This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1  
CC polynucleotide AA200040. h-TREK1 is a two pore potassium channel. The  
CC polynucleotide sequence of h-TREK1 can be used to diagnose a disease or  
CC susceptibility to a disease related to expression or activity of h-TREK-1  
CC polypeptides. The methods of diagnosis may be used in the treatment of  
CC diseases including cancer, pulmonary, cardiovascular, and inflammatory  
CC diseases, pain, psychiatric disorders including depression and  
CC schizophrenia, neurodegenerative diseases including Alzheimer's, stroke,  
CC and head trauma and neurological disorders including migraine  
XX

SO Sequence 411 AA;

Query Match 97.1%; Score 2038; DB 2; Length 411;  
Best Local Similarity 96.1%; Pred. No. 2.4e-202;  
Matches 395; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTNMWMKTVSTIFLVVLYLII 60  
DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESPTTNMWMKTVSTIFLVVLYLII 60  
QY 61 GATVFKALBOPHISQRTTIVIOKQTFISQHSQVNSTEDELIOQIVAAINNGIPLGNT 120  
DB 61 GAATVFKALBOPHISQRTTIVIOKQTFISQHSQVNSTEDELIOQIVAAINNGIPLGNS 120  
QY 121 SNOISHMDLGSFFFGVITTTGFGNISPRTEGGKIFCIYALLGIPFGFLAGVGDQ 180  
DB 121 SNOISHMDLGSFFFGVITTTGFGNISPRTEGGKIFCIYALLGIPFGFLAGVGDQ 180  
QY 181 LGTIFGKGIKAVEDTIFKNNVSQTKRIISTIFILFGCVLFVALPAVIFKHEGMSALD 240  
DB 181 LGTIFGKGIKAVEDTIFKNNVSQTKRIISTIFILFGCVLFVALPAVIFKHEGMSALD 240  
QY 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVWFWIIVGLAAYFAVLSMTGDLRVIS 300  
DB 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVWFWIIVGLAAYFAVLSMTGDLRVIS 300  
QY 301 KKTKEVGFPRAAEMTANVTAEFKETRRRLSVEIYDKFORATSIKRLSALAGNHNQ 360  
DB 301 KKTKEVGFPRAAEMTANVTAEFKETRRRLSVEIYDKFORATSIVKRLSALAGNHNQ 360  
QY 361 ELTPCRRITLSVNHLSERDVLPLLKTESIYNGLTPHCAGEIAVNIENIK 411  
DB 361 ELTPCRRITLSVNHLSERDVLPLLKTESIYNGLTPHCAGEIAVNIENIK 411

RESULT 13

ID AAY30648 standard; protein; 370 AA.

XX AAY30648;  
AC AAY30648;  
XX  
DT 18-NOV-1999 (first entry)  
XX  
DE A mechanically sensitive potassium channel protein TREK-1.  
XX  
KW Mechanically sensitive potassium channel protein; TREK-1;  
KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;  
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;  
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;  
KW muscular disease.  
XX  
OS Mus sp.  
XX  
PN WO945108-A2.  
XX  
PD 10-SEP-1999.  
XX  
PF 23-FEB-1999; 99WO-FR000404.  
XX  
PR 05-MAR-1998; 98FR-00002725.  
XX



PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;  
 XX  
 DR WPI; 1999-551038/46.  
 DR N-PSDB; AAZ10607.  
 XX  
 PT New mechanically sensitive potassium channel, used to screen for specific  
 PT modulators, potential therapeutic agents for heart and nervous system  
 PT disorders.  
 XX  
 PS Claim 3; Page 23-25; 40pp; French.  
 XX  
 CC The present sequence represents a mechanically sensitive potassium  
 CC channel protein designated TREK-1. The protein is activated by  
 CC polyunsaturated fatty acids, particularly arachidonic acid, and by  
 CC riluzole. The protein is used to screen for specific modulators which are  
 CC useful for treating or preventing diseases of the heart and nervous  
 CC systems in humans and animals, e.g. epilepsy, cardiovascular disease  
 CC (arrhythmia), neurodegeneration (particularly where associated with  
 CC ischemia or anoxia), abnormalities of hormone secretion and muscular  
 CC disease. The protein itself may be used to treat these diseases.  
 CC Antibodies specific for the protein are used to detect it in tissues,  
 CC also as therapeutic inhibitors or activators  
 CC  
 XX  
 SQ Sequence 370 AA;  
 XX  
 QY Query Match 87.4%; Score 1833; DB 2; Length 370;  
 Best Local Similarity 96.7%; Pred. No. 3, 9e-181;  
 Matches 356; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
 XX  
 QY 1 MAAPDLIDPKSAQAQNSKPRISFSTKPTVLASRVESDTTNVMMKTVSTFIVVLYLII 60  
 1 MAAPDLIDPKSAQAQNSKPRISFSTKPTVLASRVESDTTNVMMKTVSTFIVVLYLII 60  
 DB 1  
 QY 61 GAIVFKALBEPHISQRTTIVIQKPIISCHSCVNSTEDLILQOVAIINNGIIPLGNT 120  
 61 GAIVFKALBEPHISQRTTIVIQKPIISCHSCVNSTEDLILQOVAIINNGIIPLGNS 120  
 DB 61  
 QY 121 SNOISHMDLGSSEFFAGTVITTTIGFQGISPRTEGKIFCIIVALLGIPFGLLAGVGDQ 180  
 121 SNOISHMDLGSSEFFAGTVITTTIGFQGISPRTEGKIFCIIVALLGIPFGLLAGVGDQ 180  
 DB 121  
 QY 181 LGTIFGKIGAKVDDTPIKMWVSQTKRIISTITFIIFGCVLPALAAIIPKHEGSAID 240  
 181 LGTIFGKIGAKVDDTPIKMWVSQTKRIISTITFIIFGCVLPALAAIIPKHEGSAID 240  
 DB 181  
 QY 241 AIFVAVITLTITIGFGDVAGSDIEYLDFFKPVVFMILVGLAYFAAVSMIGDWLRVIS 300  
 241 AIFVAVITLTITIGFGDVAGSDIEYLDFFKPVVFMILVGLAYFAAVSMIGDWLRVIS 300  
 DB 241  
 QY 301 KKTKEVEGFRRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSGIKRKLSAELAGNNQ 360  
 301 KKTKEVEGFRRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSGIKRKLSAELAGNNQ 360  
 DB 301  
 QY 361 ELTPCRRRT 368  
 361 ELTPCRRRT 368  
 DB 361  
 QY 361 ELTPCRRRT 368  
 361 ELTPCRRRT 368  
 DB 361  
 RESULT 14  
 ABR41487  
 ID ABR41487 standard; protein; 337 AA.  
 XX  
 AC ABR41487;  
 XX  
 DT 02-JUN-2003 (first entry)  
 XX  
 DE Human DITHP membrane transport protein.  
 XX  
 KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
 KW cancer; cell proliferative disorder; autoimmune disorder;  
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;

KW neurological disorder; gastrointestinal disorder; transport disorder;  
 KW connective tissue disorder; drug screening; proteome analysis;  
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
 KW disease model; toxicological testing; transcript imaging;  
 KW membrane transport protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200297031-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 27-MAR-2002; 2002WO-US010056.  
 XX  
 PR 28-MAR-2001; 2001US-0279619P.  
 XX  
 PR 29-MAR-2001; 2001US-0280067P.  
 XX  
 PR 29-MAR-2001; 2001US-0280068P.  
 XX  
 PR 16-MAY-2001; 2001US-0291280P.  
 XX  
 PR 17-MAY-2001; 2001US-0291829P.  
 XX  
 PR 17-MAY-2001; 2001US-0291849P.  
 XX  
 PR 19-JUN-2001; 2001US-0299428P.  
 XX  
 PR 20-JUN-2001; 2001US-0299776P.  
 XX  
 PR 20-JUN-2001; 2001US-0300001P.  
 XX  
 PA (INCYTE GENOMICS INC.  
 XX  
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PP, Amthey SR;  
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstin EH;  
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
 PI Flores V, Marwana R, Lo A, Lan RY, Urahska ME;  
 DR WPI; 2003-129518/12.  
 DR N-PSDB; ACC46425.  
 XX  
 PT Novel human diagnostic and therapeutic polypeptide useful for identifying  
 PT test compound which specifically binds to a polypeptide encoded by human  
 PT diagnostic and therapeutic polynucleotide, and to induce antibodies.  
 XX  
 PS Claim 27; SEQ ID NO 1022; 591pp; English.  
 XX  
 CC The invention relates to novel human diagnostic and therapeutic  
 CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded  
 CC proteins (DITHP, ABR41136-ABR41812). The invention also relates to  
 CC polynucleotide sequences at least 90% identical to the dithp cDNA  
 CC sequences of the invention; recombinant vectors, host cells and  
 CC transgenic organisms comprising a dithp nucleic acid sequence; the  
 CC recombinant production of DITHP proteins; antibodies specific for DITHP  
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods of  
 CC detecting dithp nucleotide and protein sequences; methods of screening  
 CC for compounds which specifically bind a DITHP protein; and methods of  
 CC assessing the toxicity of test compounds using a dithp hybridisation  
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
 CC diagnosis of a wide variety of conditions including cancer and other cell  
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
 CC disorders; neurological disorders; gastrointestinal disorders; transport  
 CC disorders; and connective tissue disorders. They may also be used to  
 CC screen for modulators of protein activity or gene expression. DITHP  
 CC proteins can additionally be used in analysis of the proteome of a tissue  
 CC or cell type and to induce antibodies. The dithp nucleic acids are  
 CC additionally useful in somatic or germ-line gene therapy of the disorders  
 CC mentioned above, as a source of antisense sequences, as a source of  
 CC probes and primers, in genotyping and identification of individuals, in  
 CC the generation of transgenic animal models of human disease or knock in  
 CC humanised animals, in toxicological testing, and in transcript imaging.  
 CC The present sequence represents a DITHP protein which has membrane  
 CC transport protein activity. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pcr\_sequences  
 XX  
 SQ Sequence 337 AA;

Query Match 78.2%; Score 1641.5; DB 6; Length 337;  
 Best Local Similarity 97.0%; Pred. No. 2.6e-161;  
 Matches 322; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 80 IVIQKOTFTSQHSCVNSTEDELICQIVAINAGTIPLTGNTSNOISHWMDLSSFFPAGTV 139  
 DB 7 LVYQKHSYPTPLC-HSTBELDELICQIVAINAGTIPLTGNTSNOISHWMDLSSFFPAGTV 65  
 QY 140 ITTIGGNTSPRTGSKIFCIYIALIGPLFGFLAGVGDQIGTIFGKIAVEDTFTKM 199  
 DB 66 ITTIGGNTSPRTGSKIFCIYIALIGPLFGFLAGVGDQIGTIFGKIAVEDTFTKM 125  
 QY 200 NVSOTIRITSTIIFLFGCVLVALPATIFPKHIEGMSALDIYFVITLTIGGDYVA 259  
 DB 126 NVSOTIRITSTIIFLFGCVLVALPATIFPKHIEGMSALDIYFVITLTIGGDYVA 185  
 QY 260 GGSIDIEYLDYKPVWFILVGLAFAVLSMIGDLRVISKKTKEEVGEFFAAAEWTA 319  
 DB 186 GGSIDIEYLDYKPVWFILVGLAFAVLSMIGDLRVISKKTKEEVGEFFAAAEWTA 245  
 QY 320 NTAAREKTRRRISVYIXFORATSIKRLSABELAGNNOELTCRRTLSVNHLSERD 379  
 DB 246 NTAAREKTRRRISVYIXFORATSIKRLSABELAGNNOELTCRRTLSVNHLSERD 305  
 QY 380 VLPPILKTESIYINGLTPRCAGEBLAVIENIX 411  
 DB 306 VLPPILKTESIYINGLTPRCAGEBLAVIENIX 337

## RESULT 15

AA047930  
 ID AA047930 standard; protein; 538 AA.

AC AA047930;  
 DT 10-JUN-2002 (first entry)  
 XX Human TREK2.  
 XX Human; K<sup>+</sup> channel; potassium; TREK2; pore domain; general anaesthetic;  
 KM neurotransmitter receptor.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Domain 72..90  
 FT /note="Membrane spanning domain 1"  
 FT 152..175  
 FT /note="Pore domain 1"  
 FT 183..203  
 FT /note="Membrane spanning domain 2"  
 FT 234..255  
 FT /note="Membrane spanning domain 3"  
 FT 261..284  
 FT /note="Pore domain 2"  
 FT 300..319  
 FT /note="Membrane spanning domain 4"

PN WO200200715-A2.

PD 03-JAN-2002.

PF 27-JUN-2001; 2001WO-1B001436.

PR 27-JUN-2000; 2000US-0214559P.

PR 27-JUN-2001; 2001US-00892360.

XX (CNRS) CNRS CENT NAT RECH SCI.

PI lazdunski M, lesage F, Romey G;

XX WPI, 2002-139903/18.

DR N-PSDB: AA172558.

XX New mammalian K<sup>+</sup> channel protein with two pore domains, for screening  
 PT various compounds, particularly for identifying biologically active  
 PT compounds with anaesthetic properties.

PS Claim 3; Page 44-46; 50pp; English.

CC This sequence shows a protein, which constitutes a human K<sup>+</sup> channel,  
 CC TREK2, which has two pore domains that produces currents whose current-  
 CC voltage relationship is slightly inwardly rectifying in high symmetrical  
 CC K<sup>+</sup> conditions. TREK2 is activated by general anaesthetics at clinical  
 CC concentrations. It is modulated by different types of neurotransmitter  
 CC receptors. The TREK2 gene produces a cDNA of 2730 bp which contains an  
 CC open reading frame of 1617 nucleotides. The TREK2 protein has the same  
 CC overall structure as previously described K<sup>+</sup> channels. It has four  
 CC membrane spanning domains (M1-M4), two pore domains (P1-P2) and an  
 CC extended loop between M1 and P1. TREK2 shares 63% identity and 78%  
 CC homology to TREK1. The chromosomal location of the TREK2 gene is 14q31.  
 CC TREK2 is useful in methods for screening various compounds. In  
 CC particular, the protein is useful in methods for identifying biologically  
 CC active compounds with anaesthetic properties

XX Sequence 538 AA;

Query Match 59.2%; Score 1242.5; DB 5; Length 538;  
 Best Local Similarity 63.5%; Pred. No. 1.3e-119;  
 Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 2 AAPDLDPKSA-----AQNKRPLSFTKPTVLAASVESPT---TINWKKTKVSTI 50  
 DB 17 AAPVCCPKSATNGQPPAPAPPTPTPLSLSSRAVVA-RMEGTSQGLQVWKKVVAI 75  
 QY 51 FLVVLVLIIGATVFAKLEQPHISORTIIVIQKTFISQHSCVNSTEDELICQIVAAI 110  
 DB 76 FVVVVVLYLVGAVFPALEBPFPSSQKNTIALEKAFLELDHCVSQELETTLIQALDAD 135  
 QY 111 NAGTIPGNTSNOISHWMDLSSFFPAGTVITTTIGFENISPRTEGKIFCIYIALIGPLF 170  
 DB 136 NAGTIPGNTSNOISHWMDLSSFFPAGTVITTTIGFENISPRTEGKIFCIYIALIGPLF 195  
 QY 171 GFLLAGVGDQIGTIFGKIAKVEDTFTKNNVSQTKIRISTITIFLFGCVLFPALPAIF 230  
 DB 196 GFLLAGVGDQIGTIFGKIAKVEDTFTKNNVSQTKIRISTITIFLFGCVLFPALPAIF 255  
 QY 231 KHIEGMSALDAIFVVIITLTIGGDYVAGG-SDIEYLDYKPVWFILVGLAFAVLA 289  
 DB 256 KYIEGMSALDAIFVVIITLTIGGDYVAGG-SDIEYLDYKPVWFILVGLAFAVLA 315  
 QY 290 SMTGDMLRVTSKKTKEEVGEFFRAHAEMWTANTYAEKTRRRRLSVIYKFORATSI--- 346  
 DB 316 SMTGDMLRVTSKKTKEEVGEFFRAHAEMWTANTYAEKTRRRRLSVIYKFORATSI--- 375  
 QY 347 -KRLSABELAGNNOELTCRRTL 369  
 DB 376 ERRRLGDDQRAHSLDMLSPKRSV 399

Search completed: July 15, 2004, 17:59:23  
 Job time : 56 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 15, 2004, 17:58:13 ; Search time 16 Seconds  
(without alignments)  
2470.920 Million cell updates/sec

Title: US-09-980-350-2  
Perfect score: 2098  
Sequence: 1 MAAPDLLDPKSAQNSKPR.....LNGTTPHCAGEEIAVIENIK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Maximum Match 100%  
Listing first 45 summaries

```
Database :
1: pir_78:*
2: pir2:*
3: pir3:*
4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Match | Length | DB | ID      | Description        |
|------------|-------|-------|--------|----|---------|--------------------|
| 1          | 379.5 | 18.6  | 336    | 2  | S65566  | inward rectifier   |
| 2          | 347.5 | 16.1  | 330    | 2  | JC7703  | TSK-5 protein -    |
| 3          | 334.5 | 16.4  | 329    | 2  | T43509  | probable potassium |
| 4          | 331.5 | 15.8  | 336    | 2  | T123347 | outward rectifier  |
| 5          | 319   | 15.2  | 1001   | 2  | T13807  | potassium channel  |
| 6          | 288   | 13.7  | 383    | 2  | T23182  | potassium channel  |
| 7          | 284.5 | 13.6  | 334    | 2  | T19860  | hypothetical prot  |
| 8          | 284.5 | 13.6  | 364    | 2  | T43361  | probable potassium |
| 9          | 283.5 | 13.5  | 461    | 2  | T43394  | potassium channel  |
| 10         | 279   | 13.3  | 393    | 2  | T25392  | hypothetical prot  |
| 11         | 273   | 13.0  | 392    | 2  | T45032  | hypothetical prot  |
| 12         | 273   | 13.0  | 1910   | 2  | H88124  | protein T12C9.3 [  |
| 13         | 269   | 12.8  | 325    | 2  | T15584  | hypothetical prot  |
| 14         | 265.5 | 12.7  | 522    | 2  | T24262  | hypothetical prot  |
| 15         | 262   | 12.5  | 452    | 2  | T21116  | hypothetical prot  |
| 16         | 248.5 | 11.9  | 427    | 2  | T27681  | hypothetical prot  |
| 17         | 247   | 11.8  | 444    | 2  | T26229  | hypothetical prot  |
| 18         | 245.5 | 11.7  | 1539   | 2  | T30037  | hypothetical prot  |
| 19         | 244.5 | 11.7  | 513    | 2  | T28933  | hypothetical prot  |
| 20         | 240   | 11.4  | 524    | 2  | T23907  | hypothetical prot  |
| 21         | 236   | 11.2  | 643    | 2  | T26616  | hypothetical prot  |
| 22         | 232   | 11.1  | 528    | 2  | T21834  | hypothetical prot  |
| 23         | 230   | 11.0  | 443    | 2  | T21598  | hypothetical prot  |
| 24         | 230   | 11.0  | 550    | 2  | T23557  | hypothetical prot  |
| 25         | 228.5 | 10.9  | 484    | 2  | T45529  | probable potassium |
| 26         | 228.5 | 10.9  | 519    | 2  | T16629  | hypothetical prot  |
| 27         | 224   | 10.7  | 1336   | 2  | T26953  | hypothetical prot  |
| 28         | 220.5 | 10.5  | 551    | 2  | T16426  | hypothetical prot  |
| 29         | 220.5 | 10.5  | 555    | 2  | T43557  | potassium channel  |

|    |       |      |     |   |        |                    |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 218   | 10.4 | 307 | 2 | H89074 | protein twk-24 [im |
| 31 | 218   | 10.4 | 485 | 2 | T24201 | hypothetical prote |
| 32 | 217.5 | 10.4 | 335 | 2 | S44635 | f22b7.7 protein -  |
| 33 | 217.5 | 10.4 | 544 | 2 | T43364 | potassium channel  |
| 34 | 217.5 | 10.4 | 576 | 2 | T43363 | potassium channel  |
| 35 | 217.5 | 10.4 | 611 | 2 | S46585 | outward-rectifier  |
| 36 | 217   | 10.3 | 475 | 2 | T27725 | hypothetical prote |
| 37 | 215.5 | 10.3 | 586 | 2 | T21683 | hypothetical prote |
| 38 | 211   | 10.1 | 533 | 2 | T21551 | hypothetical prote |
| 39 | 206.5 | 9.8  | 503 | 2 | T23373 | hypothetical prote |
| 40 | 205.5 | 9.8  | 381 | 2 | T43393 | potassium channel  |
| 41 | 205.5 | 9.8  | 765 | 2 | T27550 | hypothetical prote |
| 42 | 205   | 9.8  | 700 | 2 | T27364 | hypothetical prote |
| 43 | 202.5 | 9.7  | 539 | 2 | T21700 | hypothetical prote |
| 44 | 196   | 9.3  | 681 | 2 | T13429 | hypothetical prote |
| 45 | 195   | 9.3  | 504 | 2 | T22269 | hypothetical prote |

## ALIGNMENTS

```

RESULT 1
S65566
inward rectifier potassium channel TWIK-1 - human
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S65566
R:Release: F.; Guillemaire, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanin,
EMBO J. 15, 1004-1011, 1996
A:Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel s
A:Reference number: S65566; MUID:9618184; PMID:8605869
A:Accession: S65566
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-336 <LES>
A:Cross-references: EMBL:U03632; NID:G1086490; PIDD:AMB01688.1; PID:G1086491

```

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 18.1%;           | Score 379.5;       | DB 2;      | Length 336; |
| Best Local Similarity | 32.5%;           | Pred. No. 2.4e-23; |            |             |
| Matches 90;           | Conservative 62; | Mismatches 108;    | Indels 17; | Gaps 9;     |

```

Cy      5  TLVV--VYVILIGAVYFKALTEOPHISQRTIIVIQKOFISQSCNSVSTEDILQOIVA 108
Db      25  FLVGLGILLIVGAVVSSVELEPYDILRGRIKIKRFFLEHCHCSEQQBLQGLAVLE 84
Cy      109  AINAGIIPLGNTSNQISHWLDGSSFFPAQVITTTIGFNISPRTEGGKIFCIYALIGIP 168
Db      85  ASNYGVSVLSNAGN--MMDFTSALFFPASTVLTGTGHTPLSDGKAFELIYVIGIP 143
Cy      169  LRFGLLAGVGDQGTGTFGKGIKAVEDFTIKMNVSGTKRIILSTII--FILGCLFPAALP 226
Db      144  FTLLFPLTAAVQRITVHVT--RPVYIFHHRMGESQVAVIAHVALGLGVYSCFFEL--P 199
Cy      227  AIIFFKIE--GWSALDAIYFVVTITTTIGFGDVAG--GSDIEYDLGYKPVVWFILVGLAY 284
Db      200  AAVFSVLEDDMNPLESFVFCFISLTIGLDGVDPGEVQKQRFELYKIGITCYLLGLIA 259
Cy      285  FAAVLSMIGMLRVISK-----KTGEVGEFPAHAAE 316
Db      260  MLVYLETFCE--LHELKKRKFMYKKKDQEDQVHILE 295

```

## RESULT 2

TASK-5 protein - human  
C.Species: Homo sapiens (man)  
C.Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
C.Accession: J07703  
Rikim, D.; Gnatenko, C.  
Biochem. Biophys. Res. Commun. 284, 923-930, 2001  
Article: TASK-5, a new member of the tandem-pore K<sup>+</sup> channel family.  
A.Reference number: J07703; PMID:21303050; PMID:11409881  
A.Accession: J07703

A:Molecule type: DNA  
 A:Residues: 1-330 <KIM>  
 A:Cross-references: GB:AL118522  
 C:Comment: This protein, a new member of the tandem-pore K<sup>+</sup> channel family with four transmembrane segments, but does not produce a functional plasma membrane K<sup>+</sup> current by itself  
 C:Genetics:  
 A:Gene: task-5  
 A:Map position: 20q12  
 C:Keywords: transmembrane protein  
 F:7-30/Domain: transmembrane segment #status predicted <TMS1>  
 F:107-128/Domain: transmembrane segment #status predicted <TMS2>  
 F:129-155/Region: hydrophobic cytoplasmic linker #status predicted  
 F:156-180/Domain: transmembrane segment #status predicted <TMS3>  
 F:220-240/Domain: transmembrane segment #status predicted <TMS4>

Query Match 16.6%; Score 347.5; DB 2; Length 330;  
 Best Local Similarity 34.9%; Pred. No. 9,8e-21;  
 Matches 91; Conservative 42; Mismatches 95; Indels 33; Gaps 9;

QY 50 IFLVVLVLLIGATVFKALEOPHEISQRTTIVIOKQTFISQ--HSCVNSTELDELIOOI 106  
 DB 11 LVLCICVLVGAFAVDALSEAE-SGRQLVQKRGALRRKFGSABDYRELRLALQ- 68  
 QY 107 VAAINAGIPLGNTSQISHMDIGSSFFAGVITTTIGGNSPTREGKIFCIYALIG 166  
 DB 69 AEPHRAQ-----RQMKFPGSFYFAITVITTTIGYGAHAFGIDSKYFCMFYALIG 117  
 QY 167 IFLFGLVAGVDQGTIFGKIAKVEDTF-IKMNVSQTKIRITITIFLFGCVLPAVAL 225  
 DB 118 IFLVLTPOSLGERLNAVVRLLAKCGLGRMCVSE---NLVAVGLACATLAL 173  
 QY 226 PAIFHIGMSALDAIYFVITTTIGGDIYVAGSDIEYDFKPVWF--WILVGL 282  
 DB 174 GAVAFHFGQMTFFHAYVYCFITLTITIGDFVALQSG-EALQKLPVAFSEFYLLIGL 232  
 QY 283 AYFAAVLSMI-----GDW 295  
 DB 233 TVIGAFNLVLRFLVASADW 253

RESULT 3  
 T43509  
 probable potassium channel chain n2p38 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000  
 C:Accession: T43509  
 R:Wang, Z.W.; Salikoff, L.  
 submitted to the EMBL Data Library, August 1998  
 A:Description: Potassium channels in C. elegans.  
 A:Reference number: Z22450  
 A:Accession: T43509  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-329 <WAN>  
 A:Cross-references: EMBL:AF083652; PIDN:AAC32863.1

Query Match 16.4%; Score 345; DB 2; Length 329;  
 Best Local Similarity 33.7%; Pred. No. 1.6e-20;  
 Matches 93; Conservative 56; Mismatches 93; Indels 34; Gaps 11;

QY 42 MKKTVSTIFLVV--VLYLIIGATVFKALEOPHEISQRTTIVIOKQTFISQSCVNSTEL 99  
 DB 1 MKRQNIKRLISLIVCTLYLVGAFAVDALTEHELQKLVQVRREKTKTKYNSNA-DY 59  
 QY 100 DELIOQIVAAI--NGIIPLGNTSQISHMDIGSSFFAGVITTTIGGNSPTREGKI 157  
 DB 60 EILEATIVKSVPHKAGY-----QMKFSGAFYFAITVITTTIGYGHSTPMTDAGV 108  
 QY 158 FCIIYALIGIPLFGLVAGVDQGTIFGKIAKVEDTFIKMNVSQTKIRITITIFLIF 217  
 DB 109 FCMYALVAGIPLGLMPOSGIGERNWTFPAKLL-----RFIRAKQCIYIVSSDLIFCT 163  
 QY 218 GC-VLPAALPAIFHIGMSALDAIYFVITTTIGGDIYV--GGS--DIEYLDYF 270

DB 164 GWGGLIFGGAFFSSYENWTFDAVYCFVITLTITIGFDYVALQKRGSLQTOPEYV-FF 222  
 QY 271 KPVWFWIIVGLAFAVALISMIGDMLRVISKTKREE 306  
 DB 223 SLV---FILPGLTVISANMLL--VLRFLTMNTEDE 253

RESULT 4  
 T132347  
 outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T132347  
 R:Murray, J.; Mohdamm, P.; O'Neal, D.  
 submitted to the EMBL Data Library, September 1997  
 A:Description: The sequence of C. elegans cosmid F34D6.  
 A:Reference number: Z21153  
 A:Accession: T132347  
 A:Molecule type: DNA  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Residues: 1-336 <MUR>  
 A:Cross-references: EMBL:AF025454; PIDN:AACT1151.1; GSPDB:GN00020; CESP:F34D6.3  
 A:Experimental source: strain Bristol N2; clone F34D6  
 C:Genetics:  
 A:Gene: twk-23; CESP:F34D6.3  
 A:Map position: 2  
 A:Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match 15.8%; Score 331.5; DB 2; Length 336;  
 Best Local Similarity 32.4%; Pred. No. 2e-19;  
 Matches 93; Conservative 56; Mismatches 93; Indels 41; Gaps 12;

QY 42 MKKTVSTIFLVV--VLYLIIGATVFKALEOPHEISQ-----RTTIVIOKQTFISQS 92  
 DB 1 MKRQNIKRLISLIVCTLYLVGAFAVDALTEHELQKLVQVRREKTKTKYXN 60  
 QY 93 CVNSTELDELIOQIVAAI--NGIIPLGNTSQISHMDIGSSFFAGVITTTIGGNSPT 150  
 DB 61 MSNA-DYEILEATIVKSVPHKAGY-----QMKFSGAFYFAITVITTTIGYGHSTP 108  
 QY 151 RTEGKIFCIYALIGIPLFGLVAGVDQGTIFGKIAKVEDTFIKMNVSQTKIRIIS 210  
 DB 109 MTDAGKVFCLVLAAGIPLGLVFGOSIGERNWTFPAKLI-----RFIRAKQCIYIVSS 163  
 QY 211 TIIFLFGC-VLPAALPAIFKHIEGMSALDAIYFVITTTIGGDIYV--GGS---D 263  
 DB 164 DLIIIFCTGMOGLIFGGAFFSSYENWTFDAVYCFVITLTITIGFDYVALQKRGSLQTO 223  
 QY 264 IEYLDYFKPVWFWIIVGLAFAVALSMIGDMLRVISKTKREE 306  
 DB 224 PEYV-FPSLV--FILPGLTVISANMLL--VLRFLTMNTEDE 260

RESULT 5  
 T13807  
 potassium channel protein - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster  
 C>Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000  
 C:Accession: T13807  
 R:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.  
 Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996  
 A:Title: ORK1, a potassium-selective leak channel with two pore domains cloned from Dros.  
 A:Reference number: Z17770; PMID:97075152; PMID:8917578  
 A:Accession: T13807  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1001 <GOL>  
 A:Cross-references: EMBL:U55321; NID:g3808067; PID:g3808068; PIDN:AAC69250.1  
 C:Genetics:  
 A:Gene: ORK1  
 A:Cross-references: FlyBase:FBgn0017561  
 A:Map position: 1

[illegible]

RESULT 6  
T23182  
hypothetical protein K01D12.4 - Caenorhabditis elegans  
C|Species: Caenorhabditis elegans  
C|Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C|Accession: T23182  
R|Dobson, R.  
submitted to the EMBL Data Library, June 1996  
A|Reference number: Z19703  
A|Accession: T23182  
A|Status: preliminary; translated from GB/EMBL/DBJ  
A|Molecule type: DNA  
A|Residues: 1..383 <WTL>  
A|Cross-references: EMBL:Z75543; PIDN:CAA9871.1; GSPDB:GN00023; CESP:K01D12.4  
A|Experimental source: clone K01D12  
C|Genetics:  
A|Gene: CESP.K01D12.4  
A|Map position: 5  
A|Intons: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2

|                       |       |  |       |                                     |
|-----------------------|-------|--|-------|-------------------------------------|
| Query March           | 13.7% | Score 288  | DB 2  | Length 383                          |
| Best Local Similarity | 23.6% | Pred. No. 8  | 4e-16 |                                     |
| Matches               | 85    | Conservative   | 80    | Mismatches 127, Indels 68, Gaps 12, |
| Qy                    | 20    | LSFSTKPTVLASRVESDTTINVMKKT-VSTIPLVAVLYLITIGATVPALQPHISQRT    | 78    |                                     |
| Db                    | 16    | LRANTLPBITRAKYGFARLRYYENARFVILICILLIYALFGALLFMLEMENVEDRRI    | 75    |                                     |
| Qy                    | 79    | TI---VIGKQPFISQSCVNSTELDELLQOIVAAINAGITPLGNTSQISMDGSSPEF     | 135   |                                     |
| Db                    | 76    | AIDNRMAKYQKYCYCHKPLNECDPEEMARFLISDAGTSGL-----NRSRPFDHGSLFF   | 129   |                                     |
| Qy                    | 136   | AGTVITTTGFGNISPTREBQKTFCLIVALLG---IPLFGHLLAGVDQLGTIFEGKIAT   | 191   |                                     |
| Db                    | 130   | SATVISTIGFGSTERTHIGRIITIVYGVGCTCCVLEFFNPLF---ERLVGMSYIIRS    | 185   |                                     |
| Qy                    | 192   | VEDTFIKNNVSQTKRISTII-----                                    | 223   |                                     |
| Db                    | 186   | LRERIRIRLRKSGKQKPTVLLNNEDFNESSSCGHNDMMRSPYKXFFILFISGCVLI     | 245   |                                     |
| Qy                    | 224   | ALPALIFKHIEGMSALDAIVFYVITLTITIGEDYVYAGSDIEYL---DYKYVYVFWIIVG | 281   |                                     |
| Db                    | 246   | TASAGIYVVEWENWVIDSLYFCFISFATIGFEDYVNSQODVTRMSPDLYRFNFPCLLTIG | 305   |                                     |

```

Ox      28 LAEF-----AAVISMIDLRIVSKTKKEVGFFRHAEMTANTYAETKERRRLSV 33 4
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      306 ACFFYCLSNVSSIVVRQLINM--IKKDVKY-EDRSFLC-----FKKKRRIMGL 352

RESULT 7
T19860
Hypochemical protein C4OC9.1 - Caenorhabditis elegans
C|Species: Caenorhabditis elegans
C|Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C|Accession: T19860
R|Hemby, C.
submitted to the EMBL Data Library, March 1996
A|Reference number: Z19188
A|Accession: T19860
A|Status: preliminary; translated from GB/EMBL/DDBJ
A|Molecule type: DNA
A|Residues: 1-334 <ML>
A|Cross-references: EMBL:Z70266; PIDN:CMA94204.1; GSPDB:GN00028; CBSP:C4OC9.1
C|Experimental source: clone C4OC9
C|Genetics:
A|Gene: CBSP:C4OC9.1
A|Map position: X
A|Intons: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

```

[illegible]

```

RESULT 8
T43361
Probable potassium channel chain n2p20 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C/Accession: T43361
R/Mang, Z.W.; Salkoff, L.
Submitted to the EMBL Data Library, August 1998
A/Description: Potassium channels in C. elegans.
A/Reference number: Z22450
A/Accession: T43361
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-364 <MAN>
A/Cross-references: EMBL:AF083646; PIDN:AAC32857.1

Query Match      13.6%; Score 204.5; DB 2; Length 364;
Best Local Similarity 27.4%; Pred. No. 1,5e-15;

```

Matches 86; Conservative 63; Mismatches 112; Indels 53; Gaps 11;

QY 50 IFIVVLYLIGATVFALEQPHISQRTIV---IQKOTFISQSCVNSTELDELIOOI 106  
 Db 14 LILSTFYLIFGAMVDKLE-----SEKLTWDEIERITDRKHK-YNFSERDHLFPA 67  
 QY 107 VAAINAGIILPGLTNSQISH-WDLGSSFFPAGVITTTIGFNGISPRTEGGKIFCIITALL 165  
 Db 68 IA-----IKSIPOAGQWQFAGAFYATVITTVGYSAPSTNGKIFCIITALL 119  
 QY 166 GILPFGFLAGVDQDGTIFGKIAVVEDTFK-----WNSQTKIRIIS-TTIFILFG 218  
 Db 120 GVEMGLIMFQSIERVTFLAVSLHKFRDLSHQGFTCLQEVYTPHTLWVSLTIGFMV-- 177  
 QY 219 CVLFAVLPALIFKHIGMSALDAIFVVTITLTIGFGDYV--AGSGDIEYLDFFKPVWF 276  
 Db 178 ----YSGTVMFTTIKMSIFDLYVTCMTITFTIGGDLVPLQVNALDQDLYVPATIM 233  
 QY 277 WILVGLAYFAAVISMTIGDLRVISKTKKEVGFRAHAAMWTANTAEFKETRRRLSVEI 336  
 Db 234 FILIGLAVFSACVNL-----VLGFMASNADEVTA-----AQREPPSAIV 273  
 QY 337 YDKFORATSIKRL 350  
 Db 274 LERFTNRLVDSOI 287

## RESULT 9

T43394  
 potassium channel chain n2p18 homolog - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000  
 C/Accession: T43394  
 R/Kunkel, M.T.; Salcoff, L.  
 submitted to the EMBL Data Library, August 1998  
 A/Description: Potassium channels in C. elegans.  
 A/Reference number: Z22479  
 A/Accession: T43394  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-461 <XUN>  
 A/Cross-references: EMBL:AF083650; PIDN:ACG32861.1

Query Match 13.5%; Score 283.5; DB 2; Length 461;

Best Local Similarity 23.5%; Pred. No. 2,4e-15;

Matches 102; Conservative 69; Mismatches 134; Indels 129; Gaps 14;

QY 46 TVSTIF-----LVVLYLIGATVFALEQPHISQRTIVIQKOTFISQSCVN 95  
 Db 10 TILTFQKTFKGLPLIIVATLLGAWIFWMEGSE-----REMIEGQK--- 56  
 QY 96 STELDLILQOIYVAIN-----AGIIPGLTNSQIS 125  
 Db 57 --ERDELIRRTYKINQLOIKQORLMTAEERYNRTAKVLTTFORTIGIVPA--DMDCDI 112  
 QY 126 HMDLGSSFFPAGVITTTIGFNGISPRTEGGKIFCIITALL;PLFGFLAGVDQDGTIF 185  
 Db 113 HMFPLGSIFTCMIVTTIGVNIIVPOTGKRATILYXIG;PLVLSLY-----CLGSLF 166  
 QY 186 GKCIAYVEDTFIKVANSQTKIRIIS----- 210  
 Db 169 AGCKKMLMRFLEK-----STRVSSDLNSKNISEADNIEGTATITPSAEKTENNDDDL 222  
 QY 211 ----TIFILFGCVLPALIPALIFKHIGMSALDAIFVVTITLTIGFGDYVAGSDIEYL 267  
 Db 223 LSPFIIGLLIIVYIWFCAVLEFTPIEBMDFGTSLYFTLISFTTIGFGDILP--SDYDFM 280  
 QY 268 DFYKPVVWMIIVGLAYFAVLSMTIGDLRVISKTKKEVGFRAHA-----AEWTAN 320  
 Db 281 ----PIVGVLLIIGLSLVSTVMTLLIOQIEALASGKMDKIDQEVARALNEARDEVDENH 336  
 QY 321 VNAEFETRRRLSVELYDKFORATSIKRLSLAELAGNNHQLTP-----CRRTLSVNH 374

Db 337 VDPEDEPNKKSFDAV--ISRMWMSKGLYLLPDSQKELAKOSEKMGKRSIKIQ-- 392

QY 375 TSEPDVLPPLIKTE 388

Db 393 -TDNDLLETLIRRE 405

## RESULT 10

T25392  
 hypothetical protein T29A8.1 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C/Accession: T25392  
 R/Lloyd, C.  
 submitted to the EMBL Data Library, March 1997  
 A/Reference number: Z20027  
 A/Accession: T25392  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-393 <WLL>  
 A/Cross-references: EMBL:Z92813; PIDN:CAB07286.1; GSPDB:GN00021; CESP:T29A8.1  
 A/Experimental source: clone T29A8  
 C/Genetics:  
 A/Map position: 3  
 A/Introns: 73/1; 112/3; 209/3; 287/2; 310/3; 364/2

Query Match 13.3%; Score 279; DB 2; Length 393;

Best Local Similarity 27.0%; Pred. No. 4,7e-15;

Matches 81; Conservative 54; Mismatches 107; Indels 58; Gaps 9;

QY 44 WKTIVSTIFL-----VVVLYLIGATVFALEQPHISQRTIV---IQKOTFIS--- 89  
 Db 4 WKTARILIAVSLIVLVVYVGFAGFLFYOLEQPHVEVFRANIRFNHKSQMEHLM 63  
 QY 90 --QHSQVNSHDELILQOIYVAINAGIIPLGNT-----SNQISHMDLGSSFF 135  
 Db 64 EMRESGIGQVVEDLAVKYVDNVTIRLFAFDHICGAKHLRGSGEDDNYMTALTF 123  
 QY 136 AGVITTTIGFNGISPRTEGGKIFCIITALL;PLFGFLAGVD-----QLGTIFGKG 188  
 Db 124 TTTLLTIGVGNLPTVGRKLCILYALFGVPLILITVADIGKFLSENIYQLTYWRKL 183  
 QY 189 IAKVEDFIFKVNNSQTK-----IRISTTIFILFGCVL-EVALPAILFKHI 233  
 Db 184 REKCSKQ--KYSVISSKDDKNKXEGDNLDELNYISIPILIVAILLSYITFGAVALSNW 241  
 QY 234 EGMSALDAIFVVTITLTIGFGDYVAGSDIEYLDFFKPVVWMIIVGLAYFAVLSMTIG 293  
 Db 242 EGMDFSGFPPFSRITMTTVGFDIVPLKREYILDL-----CYITIGSITTMCTIDV 295

## RESULT 11

T45032  
 hypothetical protein Y39B6.f [imported] - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
 C/Accession: T45032  
 R/Milston, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berke, M.; Bonfield, J.; Burton, R.; Faser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johns, B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D.  
 Nature 368, 32-38, 1994  
 A/Authors: Showkhen, R.; Sims, M.; Smaadon, N.; Smith, A.; Smith, M.; Sonhammer, E.; S  
 lock, L.; Wilkinson-Sproat, J.; Mohlman, P.  
 A/Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.  
 A/Reference number: S43531; M01D:94150718; PMID:7906398  
 A/Accession: T45032  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-392 <WLL>  
 A/Cross-references: EMBL:AL139896; NID:96434440; PIDN:CAB60911.1; PID:96434446  
 A/Experimental source: clone Y39B6  
 C/Genetics:

A:Map position: 3  
 A:Intons: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3  
 A:Note: Y39B6B.f

Query Match 13.0%; Score 273; DB 2; Length 392;  
 Best Local Similarity 25.5%; Pred. No. 1.4e-14;  
 Matches 83; Conservative 66; Mismatches 100; Indels 76; Gaps 13;

7 LDRKSAQNS-----KPLRSFSTKPYLAS---RVESDTINVMKKTAVSTFLVVLV 57  
 64 LERHSKQSLYVEKKAIAKEMSPYDQKTPKHFPSLTKISLKAQKRY----- 117  
 58 LIIGATVFKALEOPHEISORTTIVIOKOTFISQHS-----CVNSTELDELIOQI-V 107  
 118 -----FSRIEYPLE-----KIBREAYLDYQONWBRDLQDIDSEIDLPFINRE 163  
 108 AAINAGIIPUGNTSNQISHDLDSSFPFAGTIVTTIGFQNISPRITGKIFCIYALGLI 167  
 164 AALNGIMDMRNLTD--PNMTFQQAFFAGTLISTVGYGVSPREYKGLFTILYCVIGI 221  
 168 PLFGFLAGV-----GDQGTIFGKGIKAKVEDTFIKMVSQTKIRLISIT 212  
 222 PLTLALISAIVAMRSHKRLGLNORLGHF-----TNHIQILHVG 265  
 213 IFILFGCVLFV-ALPAIIFPHIE-GMSALDAIFVVIITLTIGFDYVAGS-DIEYIDF 269  
 266 V-VFASILLFVFALPAMVFSSIEFDWSYLDAPFYCFVSLTTIGLDFEFGDDPNQSFRL 324  
 270 YKPVVFWMLVGLAYFAAVLSMIGD 294  
 325 YKIGATVYLMGGLCCMMFLATLYD 349

RESULT 12  
 H88124  
 C:Species: Caenorhabditis elegans  
 C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #ext\_change 10-May-2001  
 C/Accession: H88124  
 R:Anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998  
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
 A:Reference number: A75000; PMID:99069613; PMID:9851916  
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele  
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
 A:Accession: H88124  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1910 <STO>  
 A:Cross-references: GB:chr\_II; PIDN:AC71141.1; PID:gl086770; GSPDB:GN00020; CESP:T12C9.3  
 A:Note: proline-rich  
 C:Genetics:  
 A:Gene: T12C9.3  
 A:Map position: 2

Query Match 13.0%; Score 273; DB 2; Length 1910;  
 Best Local Similarity 23.3%; Pred. No. 9.8e-14;  
 Matches 104; Conservative 74; Mismatches 122; Indels 146; Gaps 18;

18 PRLS--FSTKPYLAS-RVESDTI--NVMKKTAVSTFLVVLV-----LYLIGATVFA 67  
 162 PQSSRRRSIFPGLLESARPDDETTTLQNIKXAKALPHIVVVCIVATIGAMIFVT 221  
 68 LREQPHE-----ISQRTTIVIOKOTFISQHSQVNSTEID-----ELI-----Q 104  
 222 LESNENRRLKETGKRTIAEKRSNLIYK--INNNEKEVWKEDIKEKMLYSEKLYAFKE 278  
 105 QIVAINAGIIFL-----GNTSNQISH-----WDLGSSFFPAG 137  
 279 QYAVSVVRITIGFGRGSYEADDETGSDSRKRRHRGNKRGDGEKMMWTTSSALFFPA 338  
 138 TVITTTFGNISRTEGKIFCIYALGLIFLFGFLAGVDGLG--TTF-----GKGLA 190

DB 339 TTMATIGNIVPVPPLGRACVAFALFGAPIAITTTIGDLGKFLSECTIMLYKMRKGS 398  
 191 KVEDTFIKM-----NVSQTKIRLISITLIFLGC 220  
 DB 399 RLDSAWKFRGLEDSISDLESASKNODSSILDMKDDEIKSEVPVLMVFII-----L 452  
 221 LFVALPAIIFHIGESALDAIFVVIITLTIGFQNDYVAGSDIEYLDYKPVVFWMLV 280  
 DB 453 LYIARGGILFSLDMSYMDAFYFSFTSLTTIGFGDIPENHD-----YAINLIYLVG 506  
 281 GLAFPAVLSMIG-----DWLRVISKTK-----EYGEFRRAH 313  
 DB 507 GLSVTTCIDLAGQYIOKIHFGKRPQGTDLLOYLKKRMLERRLAMGQGEETLRKYH 566  
 314 AAEMTANTAEFKETRRRLSVEIYDK 339  
 DB 567 AVE-----KPERQEQLOQKMEB 585

RESULT 13  
 T15584  
 C:Species: Caenorhabditis elegans  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #ext\_change 20-Sep-1999  
 C/Accession: T15584  
 R:Favella, T.  
 submitted to: The EMBL Data Library, November 1995  
 A:Description: The sequence of C. elegans cosmid C24A3.  
 A:Reference number: Z18373  
 A:Accession: T15584  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-325 <FAV>  
 A:Cross-references: EMBL:U04024; NID:G1065542; PID:G1065543; PIDN:AAA81455.1; CESP:C24A3  
 C:Genetics:  
 A:Gene: CESP:C24A3.6  
 A:Intons: 21/1; 63/3; 131/1; 193/3; 206/3

Query Match 12.8%; Score 269; DB 2; Length 325;  
 Best Local Similarity 25.1%; Pred. No. 2.4e-14;  
 Matches 86; Conservative 53; Mismatches 88; Indels 116; Gaps 11;

46 TVSTTF-----LVVVLXILGATVFALEQPHHISORTTIVIOKOTFISQHSQVN 95  
 10 TILTFQKTEKGLPLTLIVATLIGAMIFWIMIGENE-----REMLIEQOK-- 56  
 96 STELDELIOQIVAAIN-----AGIIPUGNTSNQIS 125  
 DB 57 --ERREILRRVYVYKINQIQIKRQRIMTAEEYRNRTAKVLTTFQETLGIYVA--DMOKDI 112  
 126 HMDLSSGSPFAGTYITTTIGFQNISPRITGKIFCIYALGLIFPGLIAGVQGLTIF 185  
 DB 113 HMTPLGSIFCMYVYTTIGYGNIVPGTGMGRFATILVAFIDIPLVLSLV---CLGSLF 168  
 186 GKGIKVEDTFIKMVSQTKIRIIS----- 210  
 DB 169 AKGCKMLRFLK-----STRVYSKLSNKSISDAADNIBEGTALTIPSAKTEENDD 222  
 211 --TIFILFGCVLFVALPAIIFHIGESALDAIFVVIITLTIGFQNDYVAGSDIEYL 267  
 DB 223 LSPFISGLLITIVIVICAVLFTFLEWMDGTSLYFTLLSFTTIGFGDILP--SDYDFM 280  
 268 DFYKPVVFWMLVGLAYFAAVLSMIGDWLRVIS-----KKTKE 305  
 DB 281 ---PIGVVLLILGLSVSTVMTLIOQOIEALASVRRRRKKKK 319

RESULT 14  
 T24265  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #ext\_change 18-Feb-2000  
 C/Accession: T24265

R:Wilkinson, J.  
submitted to the EMBL Data Library, March 1996  
A/Reference number: Z19866  
A/Accession: T24265  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-522 <WIL>  
A/Cross-references: EMBL:Z70036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:T01B4.1  
A/Experimental source: clone T01B4  
C/Genetics:  
A/Map position: X  
A/Introns: 95/3; 142/1; 224/3; 290/1; 458/1

Query Match 12.7%; Score 265.5; DB 2; Length 522;  
Best Local Similarity 23.4%; Pred. No. 8.4e-14;  
Matches 99; Conservative 63; Mismatches 132; Indels 129; Gaps 15;

QY 50 FLVVVLYLIIIGATVFKALEPHE-----ISQRTTIVIQKQTFISQSCVNST 98  
DB 41 LIIILIGYACLGGMVQALEVDQQLLEBAKRVRLSESSLAVNMLEHLKQMCQSGNE 100  
QY 99 LDELIIQIYVAIINAGIIPLGNTS-NOISHMDLGSSFFPAGVITTTIGGNISPRTEGKI 157  
DB 101 ----RCLELITKTFIORSDEBERGEMWDFWNSVFSATLFTTIGGNLACKTNLGR 155  
QY 158 FCIIYVALLGIPFGFLAGVD-----QLGTIFGKG 188  
DB 156 ATIIYGMIGPLMLFLKXFGELCVMAKKIQENVOQCLKQGRKKQKASSLASITSKE 215  
QY 189 IAKV-----EDTF--IKMNSQTKRIITSTIIFILPGCVLFAVLPATIFKHEGMS 237  
DB 216 MLEVPFVEPDEDDKEDTTFQLRWG-----LVIVLFPVLCSPVSPFWENMD 260  
QY 238 ALDAIFVVTITLTTFGPGYVAGSDIEYDFYKPVWFWIL--VGLAVFAVLSMIGD- 294  
DB 261 FLTAFFYFFVSLSTIFGDIIV-----DHPRTACALFVYFGLALFANVYAILQER 312  
QY 295 ----W-LRVISKTKTEVEGEFRAHAEMTANVT----- 322  
DB 313 VENQYVMALELIDQKYOELKQDMYDEDEKADKNDMPKSKPEYRGRILLQDLRSPD 372  
QY 323 AEFKETRRLS-----VEIYDXFORATSIKRLSAEL-----AGNHOELTPCRTL 370  
DB 373 LKISGGRSSSDASSVITASDEDTNHFVGRALILAEAPAPDERASNHGTQLNSC--TVS 430  
QY 371 VNH 373  
DB 431 NEH 433

RESULT 15  
T2118  
hypotheical protein F19D8.1 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C/Accession: T21118  
R/Swinburne, J.; Ainscough, R.  
submitted to the EMBL Data Library, August 1996  
A/Reference number: Z19377  
A/Accession: T21118  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-452 <WIL>  
A/Cross-references: EMBL:Z78541; PIDN:CA801740.1; GSPDB:GN00028; CESP:F19D8.1  
A/Experimental source: clone F19D8  
C/Genetics:  
A/Map position: X  
A/Introns: 31/1; 82/2; 101/3; 157/1; 197/1; 230/3; 267/2; 325/3; 356/1; 404/3

Query Match 12.5%; Score 262; DB 2; Length 452;  
Best Local Similarity 28.5%; Pred. No. 1.4e-13;

Matches 81; Conservative 50; Mismatches 121; Indels 32; Gaps 7;  
QY 42 MKKWTSTI-----FLVVVLYLIIIGATVFKALE-----QPHISQRTTIVIQKQTFIS 89  
DB 36 MKRRNVLRILGHLALYCFVVCYFAGAWVFHQLEGENETELHDKQREYAMLKQVIAK 95  
QY 90 QHSCVNSTDELIIQIYVAIINAGIIPLGK-----TSNOISHMDLGSSFFPAGVITTT 142  
DB 96 LATTENVAELNEHLRNFELRNISNLSLNDVYLIFNEPTQVPRKWTFFPSVLSFTILTT 155  
QY 143 IFGNISPRTEGKIICIIYVALLGIPFGFLAGVDQGLTFPGKIAVVEDTFIKMNS 202  
DB 156 IGYGNVTPHTQCKVFAMTIGAFGIPFLITITIDLGRFSKTXIMALVQKVSKELEKQSD 215  
QY 203 QTKIRIISTI---IFILPGCVLFAVLPATIFKHEGMS---SALDAIFVVTITLTTFG 255  
DB 216 EHLREIAEVSPLYDVLVAGLFVVFIALGSAVIFLMENQUTYFDSVITSYMSLTITIG 275  
QY 256 DYVAGSDIEYDFYKPVWFWILVGLAVFAVLSMIGMERYI 299  
DB 276 DIVP-----RRMDFLLPTL-IYTTIGMLTTLALVEQLADVFRIV 313

Search completed: July 15, 2004, 18:01:04  
Job time: 17 secs



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OM protein - protein search, using sw model

Run on: July 15, 2004, 17:55:57 ; Search time 14 Seconds

(without alignments)  
1528.631 Million cell updates/sec

Title: US-09-980-350-2

Sequence: 1 MAPDLDPKSAQNSKPRLL.....INGLTPHCGAEIAYENIK 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID         | Description        |
|------------|--------|-------------|--------|------------|--------------------|
| 1          | 2065   | 98.4        | 426    | CIW2_HUMAN | Q95069 homo sapien |
| 2          | 2044   | 97.4        | 411    | CIW2_MOUSE | P97438 mus musculu |
| 3          | 1248.5 | 59.5        | 538    | CIW1_RAT   | Q91184 rattus norv |
| 4          | 1242.5 | 59.2        | 538    | CIW1_HUMAN | P57789 homo sapien |
| 5          | 803    | 38.3        | 333    | CIW4_HUMAN | Q9HY89 homo sapien |
| 6          | 776.5  | 37.0        | 398    | CIW4_MOUSE | Q88454 mus musculu |
| 7          | 502.5  | 24.0        | 309    | CIW5_HUMAN | Q96555 homo sapien |
| 8          | 430    | 20.5        | 489    | CIW5_MOUSE | Q95079 homo sapien |
| 9          | 393    | 18.7        | 332    | CIW1_HUMAN | Q96554 homo sapien |
| 10         | 379.5  | 18.1        | 336    | CIW1_HUMAN | Q00180 homo sapien |
| 11         | 370.5  | 17.7        | 336    | CIW1_MOUSE | Q00881 mus musculu |
| 12         | 363    | 17.3        | 394    | CIW3_HUMAN | Q14649 homo sapien |
| 13         | 357.5  | 17.0        | 365    | CIW3_MOUSE | Q91158 cavia porce |
| 14         | 348    | 16.6        | 313    | CIW5_HUMAN | Q9Y257 homo sapien |
| 15         | 347.5  | 16.6        | 330    | CIW1_HUMAN | Q9H427 homo sapien |
| 16         | 347.5  | 16.6        | 374    | CIW3_HUMAN | Q9H427 homo sapien |
| 17         | 343    | 16.3        | 409    | CIW3_MOUSE | Q35111 mus musculu |
| 18         | 343    | 16.3        | 411    | CIW3_RAT   | Q54912 rattus norv |
| 19         | 328.5  | 15.7        | 237    | CIW9_RAT   | Q96008 rattus norv |
| 20         | 324.5  | 15.5        | 318    | CIW1_RAT   | Q88510 rattus norv |
| 21         | 319    | 15.2        | 1001   | ORX1_DROME | Q94526 drosophila  |
| 22         | 307.5  | 14.7        | 430    | CIW1_HUMAN | Q9H415 homo sapien |
| 23         | 304    | 14.5        | 430    | CIW1_RAT   | Q98211 mus musculu |
| 24         | 296.5  | 14.1        | 307    | CIW8_MOUSE | Q9Y212 mus musculu |
| 25         | 291.5  | 13.9        | 307    | CIW7_HUMAN | Q9Y212 mus musculu |
| 26         | 282.5  | 13.5        | 408    | CIW1_HUMAN | Q9H415 homo sapien |
| 27         | 280    | 13.3        | 405    | CIW1_RAT   | Q9H415 homo sapien |
| 28         | 278    | 13.3        | 405    | CIW1_MOUSE | Q88135 mus musculu |
| 29         | 232    | 11.3        | 320    | TKM7_MOUSE | P34410 caenorhabdi |
| 30         | 217.5  | 10.4        | 691    | TKM1_YEAST | P40310 saccharomyc |
| 31         | 159.5  | 7.6         | 443    | KCO2_ARATH | Q9F125 arabidopsis |
| 32         | 147.5  | 7.0         | 408    | KCO5_ARATH | Q9S628 arabidopsis |
| 33         | 143    | 6.8         | 246    | KCO4_ARATH | Q9FWX6 arabidopsis |

34 140.5 6.7 436 1 KCO6\_ARATH Q9SVV6 arabidopsis  
35 126.5 6.0 669 1 KCH1\_RAT Q9Z0N7 rattus norv  
36 125.5 6.0 988 1 KCH5\_HUMAN Q9EP19 rattus norv  
37 124.5 5.9 988 1 KCH5\_HUMAN Q8GCM2 homo sapien  
38 122 5.8 676 1 KCH1\_HUMAN P51787 homo sapien  
39 121.5 5.8 363 1 KCO1\_ARATH Q81B11 arabidopsis  
40 121 5.8 228 1 KWS1\_MOUSE Q10937 caenorhabdi  
41 120 5.8 660 1 KCH1\_MOUSE Q73925 squatus aca  
42 119 5.7 604 1 KCH1\_MOUSE P97414 mus musculu  
43 115 5.5 876 1 KCH8\_MOUSE P59111 mus musculu  
44 115 5.5 1102 1 KCH8\_RAT Q9W68 rattus norv  
45 115 5.5 1107 1 KCH8\_HUMAN Q96142 homo sapien

ALIGNMENTS

RESULT 1

ID CIW2\_HUMAN STANDARD; PRT; 426 AA.

AC Q95069; Q9UNE3; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore potassium channel TPCK1).

DE KCNK2 OR TREK1 OR TREK.

GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606; [1]

RN SEQUENCE FROM N.A. PubMed=10321245; MEDLINE=99254548; Pubmed=10321245;

RY Patel A.J., Honore E., Leesage F., Fink M., Romey G., Lazdunski M.; "Inhalational anesthetics activate two-pore-domain background K+ channels"; Nat. Neurosci. 2:422-426(1999).

RL [2]

RN SEQUENCE FROM N.A.

RP TISSUE-Brain;

RC Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

RL Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.; "FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.

CC -1- SUBUNIT: Homodimer (Potential).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS CHLOROFORM, HALOTHANE AND ISOFURANE.

CC -1- SIMILARITY: Belongs to the two pore domain potassium channel family.

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CC EMBL, AF129399; AAD47569.1; -

CC EMBL, AF004711; AAD01203.1; -

CC Genew, HGNC:6277; KCKN2.

DR MIM: 603219; -

DR GO: GO:0016020; C:membrane; NAS.

DR GO: GO:0015271; F:outward rectifier potassium channel activity; NAS.

DR GO: GO:0006813; P:potassium ion transport; NAS.

DR InterPro: IPR003280; K-channel 2pore.

DR InterPro: IPR001622; K-channel pore.

DR InterPro: IPR003976; K-channel.

DR PRINTS: PR01333; 2PORECHANNEL.

DR PRINTS: PR01499; TREKCHANNEL.

DR Transport; Ion transport; Ionic channel; Voltage-gated channel;

KW

KM Potassium channel; Potassium; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 61  
 FT TRANSSEM 62 82  
 FT TRANSSEM 144 170  
 FT TRANSSEM 172 192  
 FT TRANSSEM 193 223  
 FT TRANSSEM 224 244  
 FT TRANSSEM 253 283  
 FT TRANSSEM 288 308  
 FT DOMAIN 309 426  
 FT DOMAIN 378 426  
 FT DOMAIN 354 426  
 FT CARBOHYD 110 110  
 FT CARBOHYD 134 134  
 FT CONFLICT 2 16  
 FT CONFLICT 309 311  
 FT CONFLICT 391 391  
 FT CONFLICT 411 411  
 SQ SEQUENCE 426 AA; 47016 MW; 2A8A2336D409F4E CRC64;  
 Query Match 98.4%; Score 2065; DB 1; Length 426;  
 Best Local Similarity 98.8%; Pred. No. 1,4e-136;  
 Matches 406; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MAAPDLDPKSAQNSKRLSPSTKPTVLASRVESDTTINWKMKTSTIFLVVLYLI 60  
 DB 16 VAAPDLDPKSAQNSKRLSPSTKPTVLASRVESDTTINWKMKTSTIFLVVLYLI 75  
 QY 61 GATVEFALBPHEISRTTIVIOKOTFISQSCNSTEDELICQIVAINAGIIPLANT 120  
 DB 76 GATVEFALBPHEISRTTIVIOKOTFISQSCNSTEDELICQIVAINAGIIPLANT 135  
 QY 121 SNGISHMDLGSSFFAGVITITIGFNGISPRTEGKFCICIIYALLGIPFLAGVDDQ 180  
 DB 136 SNGISHMDLGSSFFAGVITITIGFNGISPRTEGKFCICIIYALLGIPFLAGVDDQ 195  
 QY 181 LGTFPEKGIAXKVEDTIRKNNVSGTKRIITIIIFLFGCVLPAIIFKHIEGMSALD 240  
 DB 196 LGTFPEKGIAXKVEDTIRKNNVSGTKRIITIIIFLFGCVLPAIIFKHIEGMSALD 255  
 QY 241 AIFEVVITITITIGFNGVYAGSDIEYLPKPVWFMIIVGLAFPAVLSMIGDLRVIS 300  
 DB 256 AIFEVVITITITIGFNGVYAGSDIEYLPKPVWFMIIVGLAFPAVLSMIGDLRVIS 315  
 QY 301 KKTKEVGEFRAHAAEMTAVTAERKTRRLSVEIYDKFQATSIKRLSAGLNQ 360  
 DB 316 KKTKEVGEFRAHAAEMTAVTAERKTRRLSVEIYDKFQATSIKRLSAGLNQ 375  
 QY 361 ELTPCRRLSYVNHLSERDVLPLKTSBIVYNGLTTPHCAGEIVIVENIK 411  
 DB 376 ELTPCRRLSYVNHLSERDVLPLKTSBIVYNGLTTPHCAGEIVIVENIK 426  
 RESULT 2  
 C1W2 MOUSE STANDARD; PRT: 411 AA.  
 AC P97438;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (Two-pore potassium channel TRK1) (TREK-1 K+ channel subunit).  
 GN KCM2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
 RC TISSUE=Brain;

RX MEDLINE=97157476; PubMed=9003761;  
 RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,  
 RA Lazdunski M.,  
 RT "Cloning, functional expression and brain localization of a novel  
 RT unconventional outward rectifier K+ channel";  
 RL EMBO J. 15:6854-6862(1996).  
 RN [2]  
 RP REVISIONS.  
 RC TISSUE=Brain;  
 RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,  
 RA Lazdunski M.,  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP ACTIVATION.  
 RX MEDLINE=99254548; PubMed=10321245;  
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.,  
 RT "Inhalational anesthetics activate two-pore-domain background K+  
 RT channels";  
 RL Nat. Neurosci. 2:422-426(1999).  
 CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.  
 CC -1- SUBUNIT: Homodimer (potential).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).  
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO  
 CC DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN  
 CC LIVER, IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,  
 CC HIPPOCAMPUS AND CEREBELLUM.  
 CC -1- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL  
 CC ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND  
 CC ISOFLURANE.  
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL; U73488; AAC53005.2; -.  
 DR MGD; MGI:109366; Kcm2.  
 DR GO; GO:0008076; C: voltage-gated potassium channel complex; IDA.  
 DR GO; GO:0005249; F: voltage-gated potassium channel activity; IDA.  
 DR GO; GO:007186; P: G-protein coupled receptor protein signalin. .; IDA.  
 DR GO; GO:0006813; P: potassium ion transport; IDA.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR003976; Trek channel.  
 DR PRINTS: PR01333; 2PORECHANNEL.  
 DR PRINTS: PR01499; TREKCHANNEL.  
 KM Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KM Potassium channel; Potassium; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 46  
 FT TRANSSEM 47 67  
 FT TRANSSEM 129 155  
 FT TRANSSEM 157 177  
 FT TRANSSEM 178 207  
 FT TRANSSEM 208 228  
 FT TRANSSEM 238 268  
 FT TRANSSEM 273 293  
 FT TRANSSEM 294 411  
 FT DOMAIN 378 411  
 FT DOMAIN 354 411  
 FT CARBOHYD 95 95  
 FT CARBOHYD 119 119  
 SQ SEQUENCE 411 AA; 45297 MW; 8F976DD103EFA05 CRC64;  
 Query Match 97.4%; Score 2044; DB 1; Length 411;  
 Best Local Similarity 96.4%; Pred. No. 4e-135;  
 Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDPTINMKMKTVSTIFLVVLYLI 60
D 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDPTINMKMKTVSTIFLVVLYLI 60
QY 61 GATVFPKALBPHEISQRTTIVIOKOTFISQHSQVNSTEIDELIQOIVAINAGIIP 120
D 61 GATVFPKALBPHEISQRTTIVIOKOTFISQHSQVNSTEIDELIQOIVAINAGIIP 120
QY 121 SNOISHMDIGSSFFPAGTITTTGFGNISPRTEGGKIFCIYALLGIPAFGLAGVQD 180
D 121 SNOISHMDIGSSFFPAGTITTTGFGNISPRTEGGKIFCIYALLGIPAFGLAGVQD 180
QY 181 LGTIFPKGIKAVKEDTPIKNNVSGTKIRIISTIFILFGCVLPAVPAVIFKAIKESMSALD 240
D 181 LGTIFPKGIKAVKEDTPIKNNVSGTKIRIISTIFILFGCVLPAVPAVIFKAIKESMSALD 240
QY 241 AIYFVITITTTIGFGYVAGGSDIEYLDYKPVVWMLVGLAFPAVLSMIGDMLRVIS 300
D 241 AIYFVITITTTIGFGYVAGGSDIEYLDYKPVVWMLVGLAFPAVLSMIGDMLRVIS 300
QY 301 KKTKEVGFPRAPAAEMTANVTAEFKETRRRLSVEIYDFORATSIKRKLSAELAGNNO 360
D 301 KKTKEVGFPRAPAAEMTANVTAEFKETRRRLSVEIYDFORATSIKRKLSAELAGNNO 360
QY 361 ELTPCRRTLSVNLTSERDYLPLKTESIYANGLTPECAGBEIAVENIK 411
D 361 ELTPCRRTLSVNLTSERDYLPLKTESIYANGLTPECAGBEIAVENIK 411

RESULT 3
C1WA_RAT STANDARD; PRT; 538 AA.
ID C1WA_RAT STANDARD; PRT; 538 AA.
AC Q9J1S4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium channel subfamily K member 10 (Outward rectifying potassium
channel protein TREK-2) (TREK-2 K+ channel subunit).
GN KONK10 OR TREK2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20298807; PubMed=10747911;
RA Bang H., Kim Y., Kim D.;
RT "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
family."
RT J. Biol. Chem. 275:17412-17419(2000).
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY
ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.
CC ACTIVATED BY AACRIDONIC ACID AND OTHER NATURAL OCCURRING
CC UNSATURATED FREE FATTY ACIDS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN THE CEREBELLUM, SPLEEN,
CC AND TESTIS.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF196965; AAF75132.1;
CC DR InterPro: IPR003280; K-channel_2pore.
CC DR InterPro: IPR001622; K-channel_pore.
CC DR InterPro: IPR003976; Trek_channel.
CC PRINTS; PRO1333; 2PORECHANNEL.

```

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DR PRINTS; PRO1499; TREKCHANNEL.
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW Potassium channel; Potassium; Transmembrane; Glycoprotein.
FT DOMAIN 1 71
FT TRANSSEM 72 92 POTENTIAL.
FT DOMAIN 154 180 PORE-FORMING 1 (POTENTIAL).
FT TRANSSEM 182 202 POTENTIAL.
FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 234 254 POTENTIAL.
FT DOMAIN 263 294 PORE-FORMING 2 (POTENTIAL).
FT TRANSSEM 299 319 POTENTIAL.
FT DOMAIN 320 338 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 538 AA; 59800 MW; 1FF33F0AA52B97E4 CRC64;

Query Match 59.5%; Score 1248.5; DB 1; Length 538;
Beet local similarity 64.6%; Pred. No. 1.1e-79;
Matches 244; Conservative 58; Mismatches 65; Indels 11; Gaps 5;

QY 2 AAPPDLDPKSA--AONSKPRLSFSTKPTVLASRVESDPT---TINMKMKTVSTIFLVVYL 56
D 2 AAPPVQCQPKSATNQHHPVRLSISRATVVA-RMEGASQSGLOTVMKMKTVVAIFVVVVV 81
QY 57 YLTIGATVFKALBPHEISQRTTIVIOKOTFISQHSQVNSTEIDELIQOIVAINAGIIP 116
D 82 YLVGVGVFRLBPFPSSQNTIALKAEFLRDHICVSPQELTLLIQHALDADNAGVSP 141
QY 117 LGNTSNOISHMDIGSSFFPAGTITTTGFGNISPRTEGGKIFCIYALLGIPAFGLAG 176
D 142 VGNSNSSHMDLSAFAFFAGTIVTTIGXNIASDTGKIFCLYVAIFGLPFLFLLAG 201
QY 177 VGDLGTTIFGKGIKAVKEDTPIKNNVSGTKIRIISTIFILFGCVLPAVPAVIFKAIKES 236
D 202 IGDOLGTTIFGKGIKAVKEDTPIKNNVSGTKIRIISTIFILAGCIVFPAVIFKAIKES 261
QY 217 SALDAIVFVVTLLTIGFGYVAGGSDIEYLDYKPVVWMLVGLAFPAVLSMIGDMLRVIS 295
D 262 TALSITIFVVTLLTIGFGYVAGGSDIEYLDYKPVVWMLVGLAFPAVLSMIGDMLRVIS 321
QY 296 LRVISKKTKEVGFPRAPAAEMTANVTAEFKETRRRLSVEIYDFORATSIKRKLKLS 351
D 322 LRVISKKTKEVGFPRAPAAEMTANVTAEFKETRRRLSVEIYDFORATSIKRKLKLS 381
QY 352 AELAGNNOELTPCRRT 369
D 382 LDQRAHSLDMLSPKRSV 399

RESULT 4
C1WA_HUMAN STANDARD; PRT; 538 AA.
ID C1WA_HUMAN STANDARD; PRT; 538 AA.
AC P57789; Q8TDK7; Q8TBX8; Q9HB59;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium channel subfamily K member 10 (Outward rectifying potassium
channel protein TREK-2) (TREK-2 K+ channel subunit).
GN KONK10 OR TREK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=20435789; PubMed=10880510;
RA Lesage F., Terrenoire C., Romey G., Lazdunski M.;
RT "Human TREK2, a 2P domain mechanosensitive K+ channel with multiple
RT Gl and Gq protein-coupled receptors."
RT J. Biol. Chem. 275:28398-28405(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C).

```

| Query | Match | Score      | DB    | Length |
|-------|-------|------------|-------|--------|
| Best  | Local | Similarity | 63.5% | 59.2%  |
| Query | Match | Score      | DB    | Length |
| Best  | Local | Similarity | 63.5% | 59.2%  |

|            |   |  |              |          |            |      |        |     |       |         |
|------------|---|--|--------------|----------|------------|------|--------|-----|-------|---------|
|            | Matches   | 244;   | Conservative | 57;      | Mismatches | 66;  | Indels | 17; | Gaps  | 5;      |
| QY         | 2   | AAPLDLPKSA-----  | -AQN         | SKPRLSFS | TKPTV      | LSRV | SDT--- | TIN | MKRTV | STI 50  |
|            |   |  |              |          |            |      |        |     |       |         |
| Db         | 17  | AAAPVCPQSKATNGQPAPAPAPPTPTPTPLRSLSSRAVVA-RMEGISQGLQTMKKTIVAI |              |          |            |      |        |     |       | 75      |
|            |   |  |              |          |            |      |        |     |       |         |
| QY         | 51  | FLVWVLYIITATVFAKALEQPEHEISORTTVIYOKOTFISQHS                  | CN           | STEL     | DELL       | IOI  | VAI    |     |       | 110     |
|            |   |  |              |          |            |      |        |     |       |         |
| Db         | 76  | FVVVVVYLVGTGIVFRALRQGFESSQKNTIALKAEFLRHVVCVS                 | PE           | LELT     | IONAL      | DAD  |        |     |       | 135     |
|            |   |  |              |          |            |      |        |     |       |         |
| QY         | 111   | NAGIIFLCNTNSQIS  | SHMD         | LS       | SFF        | PAG  | TVTTT  | FG  | NI    | SP      |
|            |   |  |              |          |            |      |        |     |       | 170     |
| Db         | 136   | NAGVSPIONSSNNSS  | SHDL         | GS       | AF         | FPAG | IVITTT | IG  | NI    | AP      |
|            |   |  |              |          |            |      |        |     |       | 195     |
| QY         | 171   | GFLLAGVDDQIGTFFG   | KGIA         | IV       | CE         | PT   | FI     | KMN | VS    | OK      |
|            |   |  |              |          |            |      |        |     |       | 230     |
| Db         | 196   | GFLLAGIDQDQIGTIFG  | KS           | IA       | VE         | KE   | VP     | FKQ | VS    | Q       |
|            |   |  |              |          |            |      |        |     |       | 255     |
| QY         | 231   | KHIGWSALDAIYFVVT   | LT           | TTT      | IG         | GD   | V      | YAG | -SD   | E       |
|            |   |  |              |          |            |      |        |     |       | 289     |
| Db         | 256   | KYIEGWTLEBISYFV  | VV           | LT       | TV         | GG   | DF     | V   | AG    | N       |
|            |   |  |              |          |            |      |        |     |       | 315     |
| QY         | 290   | SMIDGMVRYISKTKKE   | VE           | GE       | RA         | EA   | MT     | N   | V     | T       |
|            |   |  |              |          |            |      |        |     |       | 346     |
| Db         | 316   | SMIGWMLVUSKTKKE  | VE           | GE       | LA         | KA   | EA     | MT  | N     | V       |
|            |   |  |              |          |            |      |        |     |       | 375     |
| QY         | 347   | -KRKL  | SAEL         | AG       | NH         | OE   | LT     | PC  | RT    | L 369   |
|            |   |  |              |          |            |      |        |     |       |         |
| Db         | 376   | ERRRLGIDQRAHSLD  | ML           | S        | PE         | K    | RS     | V   |       | 399     |
|            |   |  |              |          |            |      |        |     |       |         |
| RESULT 5   |   |  |              |          |            |      |        |     |       |         |
| CIW4_HUMAN | ID  | CIW4_HUMAN   | STANDARD;    |          | PRT;       |      |        |     |       | 393 AA. |
| AC         | Q9NNG8;   | Q96T94;  |              |          |            |      |        |     |       |         |
| DT         | 16-OCT-2001   | (Rel. 40, Created)   |              |          |            |      |        |     |       |         |
| DT         | 16-OCT-2001   | (Rel. 40, Last sequence update)                              |              |          |            |      |        |     |       |         |
| DT         | 15-MAR-2004   | (Rel. 43, Last annotation update)                            |              |          |            |      |        |     |       |         |
| DE         | Potassium channel subfamily K member 4 (TWIK)-related arachidonic acid- |  |              |          |            |      |        |     |       |         |
| DE         | stimulated potassium channel protein (TRAAK) (Two pore K+ channel       |  |              |          |            |      |        |     |       |         |
| GN         | KT4.1).   |  |              |          |            |      |        |     |       |         |
| GN         | KCNK4 OR TRAAK.   |  |              |          |            |      |        |     |       |         |
| OS         | Homo sapiens (Human).   |  |              |          |            |      |        |     |       |         |
| OC         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;       |  |              |          |            |      |        |     |       |         |
| OC         | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.             |  |              |          |            |      |        |     |       |         |
| OX         | NCBI_TaxID=9606;  |  |              |          |            |      |        |     |       |         |
| RN         | [1]   |  |              |          |            |      |        |     |       |         |
| RP         | SEQUENCE FROM N.A. (ISOFORM 1).   |  |              |          |            |      |        |     |       |         |
| RC         | TISSUE=Brain;   |  |              |          |            |      |        |     |       |         |
| RC         | MEDLINE=20499203; PubMed=11042359;                                      |  |              |          |            |      |        |     |       |         |
| RA         | Chapman C.G., Meadows H.U., Godden R.U., Campbell D.A., Duckworth M.,   |  |              |          |            |      |        |     |       |         |
| RA         | Keisell R.E., Murdoch P.R., Randall A.D., Rennie G.T., Gloger I.S.;     |  |              |          |            |      |        |     |       |         |
| RT         | "Cloning, localisation and functional expression of a novel human,      |  |              |          |            |      |        |     |       |         |
| RL         | cerebellum specific, two pore domain potassium channel.";               |  |              |          |            |      |        |     |       |         |
| RL         | Brain Res. Mol. Brain Res. 82:74-83(2000).                              |  |              |          |            |      |        |     |       |         |
| RN         | [2]   |  |              |          |            |      |        |     |       |         |
| RP         | SEQUENCE FROM N.A. (ISOFORM 1).   |  |              |          |            |      |        |     |       |         |
| RC         | TISSUE=Frontal cortex;  |  |              |          |            |      |        |     |       |         |
| RC         | Gray A.T.;  |  |              |          |            |      |        |     |       |         |

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RT RT "Cloning of two transcripts, HKT4.1a and HKT4.1b, from the human
RT RT two-pore K+ channel gene KCNK4. Chromosomal localization, tissue
RT RT distribution and functional expression."
RL Brain Res. Mol. Brain Res. 102:18-27(2002).
CC CC
CC CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC CC POTASSIUM CHANNEL, OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC CC EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
CC CC
CC CC -1- SUBUNIT: Homodimer (Potential).
CC CC
CC CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC CC
CC CC -1- ALTERNATIVE PRODUCTS: Integral membrane protein (Potential).
CC CC
CC CC Event=Alternative splicing; Named isoforms=2;
CC CC Name=1; Synonyms=Kt4.1a;
CC CC IsoId=Q9NYG8-1; Sequence=Displayed;
CC CC Name=2; Synonyms=Kt4.1b;
CC CC IsoId=Q9NYG8-2; Sequence=VSP_006689;
CC CC
CC CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC CC family.
CC CC
CC CC -----
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CC CC entities requires a license agreement (see http://www.isb-sdb.ch/announce
CC CC or send an email to license@isb-sdb.ch).
CC CC
CC CC EMBL; AF248242; AAC31731.1; -
CC CC DR EMBL; AF247042; AAF64062.1; ALT_INIT.
CC CC DR EMBL; AF259500; AAK49389.1; -
CC CC DR EMBL; AF259501; AAK49390.1; -
CC CC DR Genew; HENC:6279; KCNK4.
CC CC
CC CC MIM; 605720; -
CC CC DR GO; GO:0005267; F:potassium channel activity; TAS.
CC CC DR GO; GO:0006813; P:potassium ion transport; TAS.
CC CC DR InterPro; IPR003280; K+channel_2pore.
CC CC DR InterPro; IPR001622; K+channel_pore.
CC CC DR InterPro; IPR008074; TPAK channel..
CC CC
CC CC PRINTS; PR01333; 2PORECHANNEL.
CC CC
CC CC PRINTS; PR01691; TRAKCHANNEL.
CC CC
CC CC K+ transport; ion transport; Ionic channel; Voltage-gated channel;
CC CC KCNK4 potassium channel; Potassium; Transmembrane; Glycoprotein;
CC CC Alternative splicing.
CC CC
CC CC FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
CC CC FT TRANSMEM 4 24 POTENTIAL.
CC CC FT DOMAIN 89 113 PORE-FORMING 1 (POTENTIAL).
CC CC FT TRANSMEM 118 138 POTENTIAL.
CC CC FT DOMAIN 139 171 CYTOPLASMIC (POTENTIAL).
CC CC FT TRANSMEM 172 192 POTENTIAL.
CC CC FT DOMAIN 197 221 PORE-FORMING 2 (POTENTIAL).
CC CC FT TRANSMEM 234 254 POTENTIAL.
CC CC FT DOMAIN 255 393 CYTOPLASMIC (POTENTIAL).
CC CC FT CARBOHYD 78 78 N-LINKED (GLCNAC...) (POTENTIAL).
CC CC FT CARBOHYD 82 82 M-LINKED (GLCNAC...) (POTENTIAL).
CC CC FT CARBOHYD 82 82 M -> MTTAPQHPFPAAPLQAGSGAGAPAPGRAM (in
CC CC FT VASPLIC 1 1 isoform 2).
CC CC
CC CC FT CONFLICT 328 328 FTId=VSP_006689.
CC CC FT SEQUENCE 393 AA; 42704 MW; 7F18B53A0A9AD57D CRC64;
CC CC
CC CC Query Match 38.3%; Score 803; DB 1; Length 393;
CC CC Best Local Similarity 51.1%; Pred. No. 7.6e-49;
CC CC Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;
CC CC
CC CC 42 MKMKIVSIPIIVVYLYLTIGATVPFALOPHEISORTITIVQXQFIIQHSQVNSTEIDE 101
CC CC DB 1 MKSTTLMLALAVLLYLVSGALVFALBPHEIQAOQREYREKFLPAHPVSDQELGL 60
CC CC
CC CC 102 LIQQTVAAINGIILPGVYNSQISH-NDIGSSFFAGVITITIGFNISPTREGKIFC 159
CC CC DB 61 LIKEVADALGGGADGETNSTSSNSASWADLGSAPFFSGITITITIGVAVLRTDGRIFC 120
CC CC
CC CC 160 IYVALGPIPLPGFLLAGVGDOLGITFGGAGIAVETPTFKNAVVSQKIIISITIFILFGC 219

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Db 121 LFVALVGLPLFGILLAAVGRLGSLNHHGCHIEAIFLKMNVHPEELRVLSAMFLILGC 180
Oy 220 VLFVALPALIFPKHIEGSAIDAIYFVITLTITTCFGDYVAGGSDIEYLDFFKPVYWFIL 279
Db 181 LLFPLTPTFPFCVWEDMSKEAIFYFVITLTITTVGFGYVAGADRPQSPAYQPLWFWIL 240
Oy 280 VGLAVPAVISMIGDMLRVISKTKKEVGEFPRAAEMTANVA 323
Db 241 LGLAVPASVLTITGNMLRVVSRKRRALMGGLTAQAAWMTGLTVA 294

RESULT 6
C1M4_MOUSE
ID C1M4_MOUSE STANDARD; PRT; 398 AA.
AC 088454;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
Db Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-
DE stimulated potassium channel protein) (TBAK).
GN KCNK4 OR TBAK.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain.
RX MEDLINE=98292450; PubMed=9628867;
RA Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
RA Lazdunski M.,
RT "A neuronal two P domain K+ channel stimulated by arachidonic acid and
RL polyunsaturated fatty acids.";
RL EMBO J. 17:3297-3308(1998).
RN [2]
RP ACTIVATION.
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.V., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.,
RT "Inhalational anesthetics activate two-pore-domain background K+
RL channels.";
RL Nat. Neurosci. 2:422-426(1999).
CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC POTASSIUM CHANNEL, OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC EXTERNAL K+ CONCENTRATIONS.
CC -1- SUBUNIT: Homodimer (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=088454-1; Sequence=Displayed;
CC Name=2; Synonyms=TBAK1, Truncated;
CC IsoId=088454-2; Sequence=VSP_006690, VSP_006691;
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT
CC DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND
CC TESTIS.
CC -1- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED
CC FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
CC CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC family.
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CC
CC EMBL; AF056492; AAC40181.1; -.
CC MGD; MGI:1298234; Kcnk4.
CC InterPro; IPR003280; K+channel_2pore.
CC InterPro; IPR001622; K+channel_pore.

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DR InterPro: IPR008074; TRAAK_channel.
DR PRINTS; PR01333; 2PORKCHANNEL.
DR PRINTS; PR01691; TRAAKCHANNEL.
KM Transport; Ion transport; Ionic channel; Voltage-gated channel;
KM Potassium channel; Potassium; Transmembrane; Glycoprotein;
KM Alternative splicing.
FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 4 24 POTENTIAL.
FT DOMAIN 89 113 PORE-FORMING 1 (POTENTIAL).
FT TRANSMEM 119 139 POTENTIAL.
FT DOMAIN 140 171 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 172 192 POTENTIAL.
FT DOMAIN 198 222 PORE-FORMING 2 (POTENTIAL).
FT TRANSMEM 235 255 POTENTIAL.
FT DOMAIN 256 398 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 63 67 KLVLE -> KAMAI (in isoform 2).
FT VARSPIC 68 398 /FTId=VSP_006690.
SQ SEQUENCE 398 AA; 43051 MW; 478A834B7B7ABE92 CRC64;
Query Match 37.0%; Score 776.5; DB 1; Length 398;
Best Local Similarity 49.8%; Pred. No. 5,3e-47;
Matches 142; Conservative 57; Mismatches 83; Indels 3; Gaps 1;
QY 42 MKKKVSTIFLVVYVLLIGATVFKALQEPHEISQRTTIVIKQFISGHSVNSTELDE 101
DB 1 MKRTLLALLALLVLLVSGALVQALQEPHEIQKQKRDGDFLRDHPVCSQSLSD 60
QY 102 LICOIVAINAGIIP--LGNTSNOISHWDLGSSFFPAGTIVTTIGFNGISPRTEGKIF 158
DB 61 FILVLEALGGGANPETSMTNSHSAWNLGSAFFSGTITTTIGYGNIVLHTDAGRLF 120
QY 159 CIYVALLGPURPFLLAGVGDQGTIFGKGIKVEDTPIKKNVSCQTKRIITITIFLFG 218
DB 121 CIFVAVVGLPLFEMLLAGVDRIGSSLRGIGHIEIFIKHVPGLVRSLSAVLFLIG 180
QY 219 CVLFVALLPAIIFKHIGMGALDAIVFVVTITTTIGGQDVAGSGDIEYDFKPVWPMFI 278
DB 181 CLIFVLLTFPFVPSYMSKSLKALIVIVITLTVGGVDPDGDGQNSPAQPLVWMI 240
QY 279 LVGLAVFAVLSMIGWLRVISKTEVEGFRAHAETAVNTA 323
DB 241 LFLGLAVFASVLTITIGNMLRAVSRRTFAEWGGLTAAQASWTGTVA 285
RESULT 7
CING_HUMAN STANDARD; PRT; 309 AA.
ID CING_HUMAN STANDARD; PRT; 309 AA.
AC Q96T55; Q9H591;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium channel subfamily K member 16 (TWIK-related alkaline pH
DE activated K+ channel 1) (2p domain potassium channel Talk-1).
GN KCKN16 OR TALK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Pancreas;
RX MEDLINE=21164727; PubMed=11263999;
RA Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G.,
RA Lazdunski M., Lesage F.;
RT "Genomic and functional characteristics of novel human pancreatic 2p
RT domain K(+) channels.";
RU Biochem. Biophys. Res. Commun. 282:249-256(2001).
RN [2]
SQ SEQUENCE FROM N.A. (ISOFORM 2).

```

```

RA Williams S.;
RU Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Outward rectifying potassium channel. Produces rapidly
CC activating and non-inactivating outward rectifier K(+) currents.
CC -1- SUBUNIT: Homodimer (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q96T55-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q96T55-2; Sequence=VSP_006699;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Highly expressed in pancreas. Not detectable
CC in the other tissues tested.
CC -1- MISCELLANEOUS: Inhibited by Ba(+2), guanine, quinidine, chloroform
CC and halothane. Activated at alkaline pH.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC family.
CC -----
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CC -----
DR EMBL; AF358909; AAK49532.1; -
DR EMBL; AL136087; CAC07336.1; -
DR Genew; HGNC:14464; KCKN16.
DR MIM; 607369; -
DR InterPro; IPR003280; K+channel 2pore.
DR InterPro; IPR001622; K+channel pore.
DR InterPro; IPR003092; TASK channel.
DR PRINTS; PR01333; 2PORKCHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
KM Transport; Ion transport; Ionic channel; Voltage-gated channel;
KM Potassium channel; Potassium; Transmembrane; Alternative splicing.
FT DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 14 34 POTENTIAL.
FT DOMAIN 98 116 PORE-FORMING 1 (POTENTIAL).
FT TRANSMEM 120 140 POTENTIAL.
FT DOMAIN 141 165 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 166 186 POTENTIAL.
FT DOMAIN 202 221 PORE-FORMING 2 (POTENTIAL).
FT TRANSMEM 238 258 POTENTIAL.
FT DOMAIN 259 309 CYTOPLASMIC (POTENTIAL).
FT VARSPIC 269 309 LRGCGAKAPRRPRGSTARAGVQVTPQDFPISKKGIS
-> RGLGVCKGASDPSGLPRPKLTISA (in isoform
2).
SQ SEQUENCE 309 AA; 34153 MW; 99C4B11EB26B0764 CRC64;
Query Match 24.0%; Score 502.5; DB 1; Length 309;
Best Local Similarity 39.0%; Pred. No. 4,6e-28;
Matches 97; Conservative 56; Mismatches 83; Indels 13; Gaps 5;
QY 47 VSTIFLVVYVLLIGATVFKALQEPHEISQRTTIVIKQFISGHSVNSTELDIQOI 106
DB 14 VLPLLAVVYVLLIGATIFOLLERQAQSRQFQLEKIRPLENTYCLDQWAMEGCVQYI 73
QY 107 VAAINAGIIPFGTNSNOISHWDLGSSFFPAGTIVTTIGFNGISPRTEGKICITVAILG 166
DB 74 MEAWKGVNPKGSTNP-SNWDGSSFFPAGTIVTTIGFNGISPRTEAQQVCVFAALG 132
QY 167 IPLFGLLAGVGDQGTIFGKGIKVEDTPIKKNVSCQTK---IRIITIFLFGCVLEV 223
DB 133 IPLNVFL---NHLGGLRAHLAIE---RWEDRRRSQVLYVGLALFTLGLTVIL 184
QY 224 ALPAIIFKHIGMSALDAIVFVVTITTTIGFGDYVAGSGDIE-YLDFYKPVVWFVILV 282
DB 185 IFPPWVSHVSGWSPFEGYFAITLTIGFGDYVGVTPDSKRYISVRSLSAAILLGL 244

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QY 283 AYPAAVLSM 291  
 DB 245 AMLATLPL 253

RESULT 8  
 C1W5 HUMAN STANDARD; PRT; 499 AA.

AC 095273;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 5 (Acid-sensitive potassium channel protein TASK-2) (TWIK-related acid-sensitive K<sup>+</sup> channel 2).  
 GN KCNK5 OR TASK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=9903043; PubMed=9812978;  
 RA Reyes R., Duprat F., Lesage F., Fink M., Salinas M., Farman N., Lazdunski M.;  
 RT "Cloning and expression of a novel pH-sensitive two pore domain K<sup>+</sup> channel from human kidney."  
 RL J. Biol. Chem. 273:30863-30869(1998).  
 CC -1- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE. OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL K<sup>+</sup> CONCENTRATIONS.  
 CC -1- SUBUNIT: Homodimer (Potential).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION IS RESTRICTED TO THE DISTAL TUBULES OR GLOMERULI.  
 CC EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.  
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, QUINIDINE AND EXTERNAL ACIDIFICATION.  
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel family.  
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 CC -----  
 CC EMBL; AF084830; AAC79458.1; -;  
 CC GeneW; HGNC:6280; KCNK5.  
 CC MIM; 603493; -;  
 CC GO; GO:0005887; C:Integral to plasma membrane; TAS.  
 CC GO; GO:0005267; F:potassium channel activity; TAS.  
 CC GO; GO:0007588; P:excretion; TAS.  
 CC GO; GO:000613; P:potassium ion transport; TAS.  
 CC InterPro; IPR003280; K+channel\_2pore.  
 CC InterPro; IPR001622; K+channel\_pore.  
 CC InterPro; IPR003092; TASK channel.  
 CC PRINTS; PR01333; ZPORECHANNEL.  
 CC PRINTS; PR01095; TASKCHANNEL.  
 CC Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KM Potassium channel; Potassium; Transmembrane; Glycoprotein.  
 FT DOMAIN 1  
 FT TRANSMEM 7  
 FT TRANSMEM 8 26  
 FT TRANSMEM 85 112 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 113 133 POTENTIAL.  
 FT TRANSMEM 134 157 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 158 180 POTENTIAL.  
 FT TRANSMEM 190 215 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 230 250 POTENTIAL.

FT DOMAIN 251 325 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 77 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 499 AA; 55130 MM; E871A7A482DDA00 CRC64;  
 Query Match 20.5%; Score 430; DB 1; Length 499;  
 Best local similarity 31.1%; Pred. No. 8,4e-23;  
 Matches 106; Conservative 61; Mismatches 120; Indels 54; Gaps 11;

QY 54 VVLLIIGATVPKALBEPHISQRTTIVIQKQFPISSGSCVNSGTDELIIQGVAAINAG 113  
 DB 12 IIFYLAIQPAIFEVLEBPHWKAKNYTQKHLNKEFPCLGPGEDKILFVVSDAAGG 71  
 QY 114 IIPKGNSTNOISHWLSSSFFPAGVITTTIGFNGNISRETKGKIFCIYALGIPLEFGL 173  
 DB 72 VALRNGQT-FNNMWNPMIPATVITTTIGYGVNAKTPAGRLFCVYGLFVGPL---C 126  
 QY 174 LAGVDDLGITTFGKAKVEDTPIKMNVSQTKRIITITFIPLFGCVLPALALIFKH 233  
 DB 127 LTVI-SALGKFFGGARAKIQFLTKRGVSLRKAQITCTVIFIVGVLVHLVTPFVMT 185  
 QY 234 EGWGLDAIYFVVITTTTIGFGDYVAG-GSDIEYLDYKPVWFWILVGLAYPAVLSMT 292  
 DB 186 EGVYIIEGLYSSFTTITIGFGDFVAGVNSAYTHALYRFVLEMLYGLAW---LSLF 241  
 QY 293 GDMRVISKTKREVEGFRAHAEWTANVTAEFKETRRRLSVETDKQATSIKKLSA 352  
 DB 242 VNW-----KVSNF-----VEVHKAIKKRRR-----RKESF 267  
 QY 353 ELAGNHNQELPCCRILSVNHLISRDV--LPPLTKRESY 391  
 DB 268 E-SSPHS-----RKALQVKGSTASKDVNIFSLSKSEFY 301

RESULT 9  
 C1W5 HUMAN STANDARD; PRT; 332 AA.

AC 096754; Q8TAM4; Q9BXD1; Q9H592;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 17 (TWIK-related alkaline pH activated K<sup>+</sup> channel 2) (2p domain potassium channel Talk-2) (TWIK-related acid-sensitive K<sup>+</sup> channel 4) (TASK-4).  
 GN KCNK17 OR TALK2 OR TASK4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Pancreas;  
 RX MEDLINE=21164727; PubMed=11263999;  
 RA Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G., Lazdunski M., Lesage F.;  
 RT "Genomic and functional characteristics of novel human pancreatic 2P domain K(+) channels."  
 RL Biochem. Biophys. Res. Commun. 282:249-256(2001).  
 RN [2]  
 RN SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Adrenal gland;  
 RX MEDLINE=21145510; PubMed=11248242;  
 RA Decher N., Maier M., Dietrich W., Gassenhuber J., Brueggemann A., Busch A.E., Steinmeyer K.;  
 RT "Characterization of TASK-4, a novel member of the pH-sensitive, two-pore domain potassium channel family."  
 RL FEBS Lett. 492:84-89(2001).  
 RN [3]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Williams S.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RP [4]  
 RP TISSUE=Lung, and Spleen;  
 RC POTENTIAL.

RX MEDLINE=22388257; PubMed=12477932;  
 RA Straussberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,  
 RA Krausner R.D., Collins F.S., Wagner L., Stetten C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.C., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheltz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Sanchez A.,  
 RA Raha S.S., Logganiello N.A., Peters G.J., Abramson R.D., Mullish S.U.,  
 RA Bosak S.A., McKernan K.J., Maller J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield A.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein U.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Outward rectifying potassium channel. Produces rapidly  
 CC activating and non-inactivating outward rectifier K(+) currents.  
 CC -1- SUBUNIT: Homodimer (potential).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q96T54-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q96T54-2; Sequence=VSP\_006700;  
 CC Note=No experimental confirmation available;  
 CC MISCELLANEOUS: Inhibited by Ba(2+), quinidine, chloroform and  
 CC halothane. Activated at alkaline pH. Activated by quinine and  
 CC isoflurane.  
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC family.  
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to erroneous  
 CC gene model prediction.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF358910; AAK49533.1; -;  
 DR EMBL; AF339912; AAK28551.1; -;  
 DR EMBL; AL136087; CAC07335.1; ALT\_SEQ.  
 DR EMBL; BC025726; AAK25726.1; -;  
 DR GeneW; HGNC:14465; KCNK17.  
 DR MIM; 607370; -;  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR003092; TASK channel.  
 DR PRINTS; PRO1333; 2PORECHANEL.  
 DR PRINTS; PRO1095; TASKCHANNEL.  
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KW Potassium channel; Potassium; Transmembrane; Glycoprotein;  
 KW Alternative splicing.  
 FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 21 43 POTENTIAL.  
 FT DOMAIN 106 124 PORE-FORMING 1 (POTENTIAL).  
 FT DOMAIN 128 148 POTENTIAL.  
 FT DOMAIN 149 179 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 180 200 POTENTIAL.  
 FT DOMAIN 211 230 PORE-FORMING 2 (POTENTIAL).  
 FT DOMAIN 244 264 POTENTIAL.  
 FT DOMAIN 265 332 CYTOPLASMIC (POTENTIAL).  
 FT CAROXYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROXYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPLIC 260 332 IKLLISOLETPRGVSCCHSSKEDPKSOSWROGDPDPSPS  
 FT HSPQGGYPPGPGNGIIOHLEPRAHAGCGDS -> SNSSS  
 FT PSMRQGGVPAATLALRTSSPKAGDRDLTQSOPTPSK  
 FT DA1ORDWESYSIMNLLTLQAIVARTASTYPPGRRPR  
 FT (in isoform 2).  
 FT /FTRID=VSP\_006700.  
 FT S -> G (IN REF. 2 AND 4).  
 FT SEQUENCE 332 AA; 36894 MW; 1648DBC06E078158 CRC64;  
 SO  
 Query Match 18.7%; Score 393; DB 1; Length 332;  
 Best Local Similarity 36.1%; Pred. No. 2e-20;  
 Matches 91; Conservative 53; Mismatches 92; Indels 16; Gaps 7;  
 QY 48 STEFLVY--LVYLLIGATVKALEQHEHISRTITVIOGFTFSQSCVNSVTELDLQ 105  
 DB 21 STVLLALVAYVALALGVWTLLEGRAQDSSSPFRDKWELLQNTCLDRPALDGLND 80  
 QY 106 IVAAINAGIIPLGNTSNOISHWLDGSPFPAGVTITTFGNIISPTEGKIPICITALL 165  
 DB 81 VQAVYKAGALLSNTTS-MGRWELVGSFPFVSITITIGVNLSPVTMARLFCIFPALV 139  
 QY 166 GIPPLFGILAGVDQCTIFGKGI---AKVETFTKNAVSOIKRITITIFILFGCVL 221  
 DB 140 GIPPLLVYLV---NRGLHMQGVNEMASRLGQT--WQ-DDPKAKWILAGSGLLSGLLT 191  
 QY 222 FVALPAIIFPGHIEGMSALDAIVFVITLTITGGDYVAGSDIE-VLDFYKPVFWFVIL 280  
 DB 192 FULLPLPLFPMHMGWSYTESGFYAFITLSTVGGDVIVAGNSQRPFLVYKNAVSWILF 251  
 QY 281 GLAVFAAVLSMI 292  
 DB 252 GWAMALLIILKI 263  
 RESULT 10  
 ID CIRM\_HUMAN STANDARD; PRT; 336 AA.  
 AC 000180; Q13307;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 1 (inward rectifying potassium  
 DE channel protein TWIK-1) (Potassium channel KONO1).  
 GN KCNK1 OR TWIK1 OR KONO1 OR KONO1.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.  
 RC TISSUE=Kidney;  
 RA Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G.,  
 RA Barhanin J.,  
 RT "TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with a  
 RT novel structure.";  
 RT EMBO J. 15:1004-1011(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND REVIEW.  
 RC TISSUE=Brain;  
 RA Goldstein S.A.N., Wang X.-W., Ilan N., Pausch M.H.,  
 RT "Sequence and function of the two P domain potassium channels:  
 RT implications of an emerging superfamily.";  
 RT J. Mol. Med. 76:13-20(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98026667; PubMed=9362344;  
 RX Clias M., Velazquez H., Tung F., Lee G., Desir G.V.,  
 RT "Cloning and localization of a double-pore K channel, KCNK1: exclusive  
 RT expression in distal nephron segments.";  
 RL Am. J. Physiol. 273:F663-F666(1997).  
 RN [4]



RP SEQUENCE FROM N.A.  
 CC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Urdan T.B., Toshiyuki S., Carninci P., Parise C.,  
 RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mallya S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guntarine P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.N., Gay L.J., Hultyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Weakly inward rectifying potassium channel.  
 CC -1- SUBUNIT: Homodimer (potential).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: Widely expressed with high levels in heart and  
 CC brain and lower levels in placenta, lung, liver and kidney.  
 CC -1- MISCELLANEOUS: Inhibited by barium, quinine, quinidine and  
 CC internal acidification. Activated by protein kinase C.  
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC family.  
 CC -----  
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 CC -----  
 DR EMBL: U36332; AAB01688.1; -  
 DR EMBL: U76996; AAB97878.1; -  
 DR EMBL: U90065; AAB5147.1; -  
 DR EMBL: BC018051; AAL18051.1; -  
 DR PIR: S65566; S65566.  
 DR GeneW: HGNC:6272; KCNK1.  
 DR MIM: 601745; -  
 DR GO: GO:0008076; C:Voltage-gated potassium channel complex; TAS.  
 DR GO: GO:0005242; F:Inward rectifier potassium channel activity; TAS.  
 DR GO: GO:0006813; P:Potassium ion transport; TAS.  
 DR InterPro: IPR003280; K+channel\_2pore.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR001779; TWIK1\_channel.  
 DR InterPro: IPR005408; TWIK1\_channel.  
 DR PRINTS: PRO1333; 2PORECHANNEL.  
 DR PRINTS: PRO1096; TWIK1CHANNEL.  
 DR PRINTS: PRO1586; TWIKCHANNEL.  
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KW Potassium channel; Potassium; Transmembrane; Glycoprotein.  
 KW DOMAIN 1 20  
 FT TRANSSEM 21 41  
 FT TRANSSEM 104 130  
 FT TRANSSEM 133 153  
 FT TRANSSEM 154 177  
 FT TRANSSEM 178 198  
 FT TRANSSEM 212 238  
 FT TRANSSEM 247 267  
 FT TRANSSEM 268 336  
 FT TRANSSEM 95 95  
 FT TRANSSEM 161 161  
 FT TRANSSEM 336 AA; 38143 MW; 2A4ID950132325D CRC64;  
 SO SEQUENCE

Query Match 18.1%; Score 379.5; DB 1; Length 336;  
 Best Local Similarity 32.5%; Pred. No. 1,8e-19;  
 Matches 90; Conservative 62; Mismatches 108; Indels 17; Gaps 9;  
 QY 51 FLVY--VLYLIGATVKALEQPHISQRTTIVQKQTFISQSCVNSTLDELICQIVA 108  
 DB 25 FLVGYLLVYFVGAVSVSELPEDLLROELRLKRFLEEHCHLSQQLQEPVGLVLE 84  
 QY 109 AINAGIPLAGTSQIQSHMDGSGFPFAGVITTTIGGNISPREGKIPCIITIALGIP 168  
 DB 85 ASNVGVSTLSASGN-NMWDPTSLFPASTYLTSTGCHVPLSDGKARCIITVSIGIP 143  
 QY 169 LFGFLAGVSDQDLTTEGKIAKVEDTFIKNVSQTKIRIISTII--FILECYLVALP 226  
 DB 144 FTLLFLAVVQRIIVHVR--RPVLYPHIRGFSKOVAVIHAVLGFVVSCEFFI--P 199  
 QY 227 AIFPHIE-GMSALDAIYFVITLTITGFGPYVG-GSDIEYLDYFVYVFWFVGLAY 284  
 DB 200 AAVSVLEDDMNFESYFCISTIGLDYVGEYNQKFRRLYKIGITCYLLGLIA 259  
 QY 285 FAAYLSMIGDLRVISK----KTKEVGEFRHAAAE 316  
 DB 260 MLVYLEFCE-LHLLKFRKMFYVKDKDEQVHIE 295  
 RESULT 11  
 ID C1W1 MOUSE STANDARD; PRT; 336 AA.  
 AC 008581;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 1 (Inward rectifying potassium  
 DE channel protein TWIK-1).  
 GN KCNK1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97165599; PubMed=9013852;  
 RA Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,  
 RT Lazdunski M.,  
 RT "The structure, function and distribution of the mouse TWIK-1 K+  
 RT channel."  
 RL FEBS Lett. 402:28-32(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvJ; TISSUE=Liver;  
 RX MEDLINE=98218573; PubMed=9559671;  
 RA Arrighi I., Lesage F., Sciamea J.-C., Carle G.F., Barhanin J.,  
 RT "Structure, chromosome localization, and tissue distribution of the  
 RT mouse twik K+ channel gene."  
 RL FEBS Lett. 425:310-316(1998).  
 CC -1- FUNCTION: Weak inwardly rectifying potassium channel.  
 CC -1- SUBUNIT: Homodimer (Potential).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: Widely expressed. Highest expression in brain,  
 CC kidney, thyroid, salivary gland, adrenal gland, prostate,  
 CC epididymis, uterus, placenta, colon and jejunum. Moderate  
 CC expression in eyes, pituitary, pancreas, smooth muscle, testis and  
 CC ovary. Very low levels in lung, aorta, liver, heart, skeletal  
 CC muscle, thymus and spleen. In the brain, highest expression in  
 CC cerebellar granule cells, brainstem, hippocampus and cerebral  
 CC cortex.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST  
 CC CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND  
 CC STABILIZES AFTER DAY 8.  
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, BARBIT, AND INTERNAL  
 CC ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.  
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel

## family.

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DR EMBL: AF03017; AAC16973.1; -  
DR MGD: MGI:109322; Kcnk1.  
DR InterPro: IPR003280; K+channel\_2pore.  
DR InterPro: IPR001622; K+channel\_pore.  
DR InterPro: IPR001779; TWIK1\_channel.  
DR InterPro: IPR005408; TWIK1\_channel.  
DR PRINTS: PR01333; 2PORECHANNEL.  
DR PRINTS: PR01095; TWIK1CHANNEL.  
DR PRINTS: PR01586; TWIK1CHANNEL.  
KM Transport; Ion transport; Ionic channel; Voltage-gated channel;  
KW Potassium channel; Potassium; Transmembrane; Glycoprotein.  
FT DOMAIN 1 20  
FT TRANSMEM 21 41  
FT DOMAIN 104 130  
FT TRANSMEM 133 153  
FT TRANSMEM 154 177  
FT TRANSMEM 178 198  
FT DOMAIN 212 238  
FT TRANSMEM 247 267  
FT TRANSMEM 268 336  
FT CARBOHYD 95  
SQ SEQUENCE 336 AA; 38275 MW; A996050A18265FD4 CRC64;

Query Match 17.7%; Score 370.5; DB 1; Length 336;  
Best Local Similarity 33.9%; Pred. No. 7.6e-19;

Matches 83; Conservative 57; Mismatches 94; Indels 11; Gaps 7;

QY 51 FLVW-VLYLIGATVFKALQEPHEISQRTTIVIOKQTFISCSVNSTELDELIQIVVA 108  
DB 25 FLVGLYGLVGVAVVFSSEELPYEDLLKQELKXKRRLFEHCELEPQLEQFLGVLE 84  
QY 109 AINAGIPIICNTSNQSHWDLGSSPPFACVTITTTGFGNISRTGSGKIFCIYVLLGIP 168  
DB 85 ASNYGVSVLSNAGN-WNWDFTSALFPASTVISTGGYGVPLSDGGKAFCLISVIGIP 143  
QY 169 LQFLLAGVGDQGLITFGKIAKVEDTFIKMNVSTQKIRIISTII--FILFGCVLVALP 226  
DB 144 FTLLFLTALVQVTVHVR--RPVLYEHIRMGFSQVAVLAVLGVTVSCFFFI--P 199  
QY 227 AIIIFKATIE-GMSALDAIYFVVTITLTIGGDYVAG-GSDIEYLDYKPVVWFMIWGLAY 284  
DB 200 AAVFVYLEDNMFLEFVFCFISLTIGDYVPEGVNOKRELKIGITCYLLGLIT 259  
QY 285 FAAYL 289  
DB 260 MLVVL 264

RESULT 12

ID C1W3 HUMAN STANDARD; PRT; 394 AA.

AC 014649;  
DT 16-OCT-2001 (Rel. 40; Last sequence update)  
DT 15-MAR-2004 (Rel. 43; Last annotation update)  
DE Potassium channel subfamily K member 3 (Acid-sensitive potassium  
DE channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)  
DE (Two pore potassium channel KTR.1).  
GN KCNK3 OR TASK1 OR TASK.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;

EN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=97459932; PubMed=9312005;  
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;  
RT "TASK, a human background K+ channel to sense external pH variations  
RT near physiological pH.";  
RL EMBO J. 16:5464-5471(1997).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RA Lopes C.M.B., Gallagher P.G., Buck M.E., Butler M.H.,  
RA Goldstein S.A.N.;  
RT "Proton block and voltage-gating are potassium-dependent in the  
RT cardiac leak channel Kcnk3.";  
RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.  
[3]  
RP ACTIVATION.  
RX MEDLINE=99254548; PubMed=10321245;  
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;  
RT "Inhalational anesthetics activate two-pore-domain background K+  
RT channels.";  
RL Nat. Neurosci. 2:422-426(1999).  
[4]  
RP MYOGENESIS OF HIS-98.  
RX MEDLINE=21535313; PubMed=11680614;  
RA Ashmole I., Goodwin P.A., Stanfield P.R.;  
RT "TASK-5, a novel member of the tandem pore K+ channel family.";  
RL Pflügers Arch. 442:828-833(2001).  
-1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM  
CC CHANNEL. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM  
CC ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN  
CC OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.  
CC WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD.  
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST  
CC EXPRESSION IN PANCREAS AND PLACENTA. LOWER EXPRESSION IN BRAIN,  
CC LUNG, PROSTATE, HEART, KIDNEY, UTERUS, SMALL INTESTINE AND COLON.  
-1- MISCELLANEOUS: INHIBITED BY EXTERNAL ACIDIFICATION. ACTIVATED BY  
CC HALOTHANE AND ISOFLURANE.  
-1- SIMILARITY: Belongs to the two pore domain potassium channel  
CC family.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).



RT (TOSS) : a novel human 2-pore K<sup>+</sup> channel principal subunit." ;  
 RL FEBS Lett. 450:191-196(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND MUTAGENESIS OF CVS-53.  
 RC TISSUE=Brain;  
 RX MEDLINE=99175162; PubMed=10075682;  
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,  
 RT Mehta Y., Forsythe J.R., Yost C.S.;  
 RT "TWIK-2, a new weak inward rectifying member of the tandem pore domain  
 potassium channel family." ;  
 RL J. Biol. Chem. 274:7887-7892(1999).  
 RN [3]  
 RP ERRATUM.  
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,  
 RT Mehta Y., Forsythe J.R., Yost C.S.;  
 RL J. Biol. Chem. 274:24440-24440(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1 AND 2), AND CHARACTERIZATION.  
 RX MEDLINE=20435832; PubMed=10887187;  
 RA Patel A.J., Malingret F., Magnone V., Fosset M., Lazdunski M.,  
 RT Honoré B.;  
 RT "TWIK-2, an inactivating 2P domain K<sup>+</sup> channel." ;  
 RL J. Biol. Chem. 275:28722-28730(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Chen A.F., Gray A.T., Chen A.H., Kindler C.H., Mhatre A.N., Yost C.S.,  
 RT Lalwani A.K., Smith R.J.H.;  
 RT "Genomic structure and mutation screening of the TWIK-2 gene." ;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Pancreas;  
 RX MEDLINE=23388257; PubMed=12477932;  
 RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 RA Altschuler S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Cantino P., Prange C.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McMan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halik S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey U., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences." ;  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC - FUNCTION: Exhibits outward rectification in a physiological K(+)   
 gradient and mild inward rectification in symmetrical K(+)   
 conditions.  
 CC SUBUNIT: Homodimer (Potential).  
 CC SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC - ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1:  
 CC IsoId=Q9Y257-1; Sequence=Displayed;  
 CC Name=2:  
 CC IsoId=Q9Y257-2; Sequence=VSP\_006692;  
 CC - TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES  
 CC TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN  
 CC PLACENTA, PANCREAS, HEART, COLON AND SPLEEN. LOWER LEVELS DETECTED  
 CC IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.  
 CC LOWEST EXPRESSION DETECTED IN BRAIN.  
 CC - MISCELLANEOUS: INHIBITED BY INTERVAL ACIDIFICATION AND, TO A SMALL  
 CC DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARBITUM.  
 CC - SIMILARITY: Belongs to the two pore domain potassium channel  
 CC family.

CC -----  
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL databank.  
 CC The European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC -----  
 DR EMBL; AF134149; AAD22980.1; -;  
 DR EMBL; AF117708; AAD24000.1; -;  
 DR EMBL; AF261302; AAG10506.1; -;  
 DR EMBL; AF261303; AAG10507.1; -;  
 DR EMBL; AJ297404; CAC15489.1; -;  
 DR EMBL; AJ297405; CAC15489.1; JOINED.  
 DR EMBL; BC004367; AAH04367.1; -;  
 DR Genem; HGNC:6281; KCNK6.  
 DR MIM; 603939; -;  
 DR GO; GO:0008076; C: voltage-gated potassium channel complex; TAS.  
 DR GO; GO:0005242; F: inward rectifier potassium channel activity; TAS.  
 DR GO; GO:0006813; F: potassium ion transport; TAS.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR001779; TWIK1\_channel.  
 DR InterPro; IPR005409; TWIK2\_channel.  
 DR InterPro; IPR005408; TWIK\_channel.  
 DR PRINTS; PR01333; 2PROKCHANEL.  
 DR PRINTS; PR01096; TWIK1CHANNEL.  
 DR PRINTS; PR01587; TWIK2CHANNEL.  
 DR PRINTS; PR01586; TWIKCHANNEL.  
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KW Potassium channel; Potassium; Transmembrane; Glycoprotein;  
 KW Alternative splicing.  
 FT DOMAIN 1 4  
 FT TRANSSEM 5 25  
 FT DOMAIN 90 115  
 FT TRANSSEM 121 141  
 FT DOMAIN 142 172  
 FT TRANSSEM 173 193  
 FT DOMAIN 199 223  
 FT TRANSSEM 236 256  
 FT DOMAIN 257 313  
 FT CARBOHYD 79 85  
 FT CARBOHYD 85 85  
 FT VARSPPLIC 1 134  
 FT FT  
 SQ MTPAGEN 53 53  
 SQ SEQUENCE 313 AA; 33747 MW; 1379382DF50575DE CRC64;  
 Query Match 16.6%; Score 348; DB 1; Length 313;  
 Best local Similarity 34.4%; Pred. No. 2.6e-17;  
 Matches 83; Conservative 42; Mismatches 104; Indels 12; Gaps 5;  
 QY 57 YLIGATVTKALQEPHEISQRTTIVQKOTFISQHSQVSTLDELIOQVAINAGIIP 116  
 DB 17 YLVGLALVARLEGPEARLRABLETLRQQLQISQCVAPADPAFVENVLAAGKRV 76  
 QY 117 LGNTSQNIS---HMDLSSFPFAGVTITIGFNGNISPTREGKIFCIYALGIPDFG 172  
 DB 77 LANASSANASDPAWDFASALFPASTLTITVGQYTPITDAGKAFSIFALLGVPITWL 136  
 QY 173 LLAGVDDQGTIGFKGIAYEDTIFKRVNSQIKRIRISITITIFIGCVLFA--LPAIF 230  
 DB 137 LITASQRIISL---LTHVPLSMRWGMDERRRAACHVALGAVVTVCPVPAVIF 192  
 QY 231 KHI-EEMSALDAIFVYVITLTIGFDVYAGSDIE-YDFYKPVVFWILVGLAYFAV 288  
 DB 193 AHLEFMSFLDAFFPFCIFLSTIGIGDYVPGAPQPVYALKVLTVTVLFGIVAMVIV 252  
 QY 289 L 289  
 DB 253 L 253



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Qy 167 IPFGFLAGVDPDQITFGKGIKAKVEDTE-IKMNVSOIKRIISTITIFILGCVLPVAL 225
    ||| :|| : : : :|| :||
Db 118 IPDLTVTPOSIGERLNAVVRRLIAKCCGLRWTCVSTE---NLVVAGLIACAATIAL 173
    ||| :|| : : : :|| :||
Qy 226 PALIFKHIEGWSALDAIYFVVTTLTTIGFDYVAGGSDIEYLDIFYKPVWF---WILVGL 282
    ||| :|| : : : :|| :||
Db 174 GAVAFSHFEGWTFEFHAYYCFITLTTIGFDVVALQSG-EALQRLPYVAFSFLYILGL 232
    ||| :|| : : : :|| :||
Qy 283 AYPFAVLSMI-----GDW 295
    ||| :|| : : : :|| :||
Db 233 TVIGAPLNLVLRFLVASADW 253
    ||| :|| : : : :|| :||

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Search completed: July 15, 2004, 17:59:46  
 Job time : 15 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 15, 2004, 17:56:18 ; Search time 39 Seconds  
(without alignments)  
3325.076 Million cell updates/sec

Title: US-09-980-350-2

Sequence: 1 MAPDLDPKSAQNSKPRLL.....LNGLTPHCAGEIAVENIK 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP virus:\*  
16: SP bacterioph:\*  
17: SP archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID  | Description        |
|------------|--------|-------------|--------|--------|--------------------|
| 1          | 2098   | 100.0       | 411    | Q9NR22 | Q9NR22 homo sapien |
| 2          | 2082   | 99.2        | 411    | Q8HY88 | Q8HY88 bos taurus  |
| 3          | 2028   | 96.7        | 426    | Q920B6 | Q920B6 rattus norv |
| 4          | 1248.5 | 59.5        | 453    | Q8BZB0 | Q8BZB0 mus musculu |
| 5          | 1248.5 | 59.5        | 535    | Q8BUW1 | Q8BUW1 mus musculu |
| 6          | 764.5  | 36.4        | 397    | Q924I4 | Q924I4 rattus norv |
| 7          | 616    | 29.4        | 241    | Q9CX88 | Q9CX88 mus musculu |
| 8          | 415    | 19.8        | 502    | Q9TK62 | Q9TK62 mus musculu |
| 9          | 413    | 19.7        | 341    | Q8BRT2 | Q8BRT2 mus musculu |
| 10         | 409.5  | 19.5        | 257    | Q8OXE0 | Q8OXE0 bos taurus  |
| 11         | 406.5  | 19.4        | 307    | Q8O1T4 | Q8O1T4 xenopus lae |
| 12         | 400    | 19.1        | 184    | Q8N4V5 | Q8N4V5 homo sapien |
| 13         | 380    | 18.1        | 336    | Q8R4S4 | Q8R4S4 cavia porce |
| 14         | 378.5  | 18.0        | 336    | Q922T2 | Q922T2 rattus norv |
| 15         | 377.5  | 18.0        | 336    | Q9S199 | Q9S199 mus musculu |
| 16         | 372    | 17.7        | 331    | Q8AV15 | Q8AV15 xenopus lae |

|    |       |      |      |    |        |                     |
|----|-------|------|------|----|--------|---------------------|
| 17 | 356.5 | 17.0 | 259  | 6  | 002821 | 002821 coryctolagus |
| 18 | 351.5 | 16.8 | 396  | 11 | Q923V6 | Q923V6 rattus norv  |
| 19 | 345   | 16.4 | 329  | 5  | 017185 | 017185 caenorhabdi  |
| 20 | 344   | 16.4 | 311  | 11 | Q8B222 | Q8B222 mus musculu  |
| 21 | 343   | 16.3 | 313  | 11 | Q9ERUS | Q9ERUS rattus norv  |
| 22 | 341   | 16.3 | 395  | 11 | Q9J1D4 | Q9J1D4 rattus norv  |
| 23 | 336   | 16.0 | 299  | 11 | Q9QX34 | Q9QX34 mus musculu  |
| 24 | 316.5 | 15.1 | 312  | 11 | Q8R4S3 | Q8R4S3 cavia porce  |
| 25 | 305   | 14.5 | 319  | 5  | Q9NEV3 | Q9NEV3 caenorhabdi  |
| 26 | 300   | 14.3 | 340  | 5  | Q9VHE0 | Q9VHE0 drosophila   |
| 27 | 299.5 | 14.3 | 343  | 11 | Q9U1I4 | Q9U1I4 mus musculu  |
| 28 | 296.5 | 14.1 | 398  | 5  | Q9VFS9 | Q9VFS9 drosophila   |
| 29 | 293.5 | 14.0 | 392  | 11 | Q9ESM5 | Q9ESM5 rattus norv  |
| 30 | 288   | 13.7 | 383  | 5  | Q21094 | Q21094 caenorhabdi  |
| 31 | 284.5 | 13.6 | 364  | 5  | Q76790 | Q76790 caenorhabdi  |
| 32 | 283.5 | 13.5 | 461  | 5  | 018120 | 018120 caenorhabdi  |
| 33 | 282   | 13.4 | 385  | 5  | Q9VY75 | Q9VY75 drosophila   |
| 34 | 279   | 13.3 | 393  | 5  | Q9XU07 | Q9XU07 caenorhabdi  |
| 35 | 277.5 | 13.2 | 426  | 5  | Q816M6 | Q816M6 aplysia cal  |
| 36 | 267.5 | 12.8 | 372  | 5  | Q7YX77 | Q7YX77 caenorhabdi  |
| 37 | 265.5 | 12.7 | 522  | 5  | Q22042 | Q22042 caenorhabdi  |
| 38 | 262   | 12.5 | 452  | 5  | Q93531 | Q93531 caenorhabdi  |
| 39 | 262   | 12.5 | 498  | 5  | Q22940 | Q22940 caenorhabdi  |
| 40 | 261.5 | 12.5 | 314  | 11 | Q8Q226 | Q8Q226 cavia porce  |
| 41 | 261.5 | 12.5 | 395  | 5  | Q9V362 | Q9V362 drosophila   |
| 42 | 250   | 11.9 | 618  | 5  | F90863 | F90863 caenorhabdi  |
| 43 | 249.5 | 11.9 | 427  | 5  | Q23386 | Q23386 caenorhabdi  |
| 44 | 247   | 11.8 | 444  | 5  | Q45891 | Q45891 caenorhabdi  |
| 45 | 245.5 | 11.7 | 1357 | 5  | Q817K7 | Q817K7 caenorhabdi  |

#### ALIGNMENTS

RESULT 1  
ID Q9NR22 PRELIMINARY; PRT; 411 AA.  
AC Q9NR22  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Two-pore domain potassium channel TREK-1.  
GN TREK-1  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20244931; PubMed=10784345;  
RA Medhurst A.D., Benham C.D., Cairns W., Gloger I.S., Jennings C.,  
RT "Cloning, localisation and functional expression of the human  
orthologue of the TREK-1 potassium channel.",  
RL Pfleger Arch. 439:714-722(2000).  
DR EMBL: AF171058; AAF89743.1;  
DR GO: GO:0016021; C: integral to membrane; IEA.  
DR GO: GO:0005216; F: ion channel activity; IEA.  
DR GO: GO:0005267; F: potassium channel activity; IEA.  
DR GO: GO:0006813; P: potassium ion transport; IEA.  
DR InterPro: IPR003280; K: potassium ion pore.  
DR InterPro: IPR001622; K: channel pore.  
DR InterPro: IPR003976; T:rek channel.  
DR PRINTS: PR01333; 2P0REKCHANEL.  
DR PRINTS: PR01499; TREKCHANNEL.  
DR Ionic Channel; Transmembrane.  
SQ SEQUENCE 411 AA; 45494 MW; FDE40CAB21842A1C CRC64;  
Query Match 100.0%; Score 2098; DB 4; Length 411;  
Best Local Similarity 100.0%; Pred. No. 2.4e-166;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINWKMKTGSTIFLVVLYLI 60
DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINWKMKTGSTIFLVVLYLI 60
QY 61 GATVFALQEPHEISORTTIVIOKOTFISQHSQVNSTELDELIOQIVAINAGIIPLCNT 120
DB 61 GATVFALQEPHEISORTTIVIOKOTFISQHSQVNSTELDELIOQIVAINAGIIPLCNT 120
QY 121 SNOISHWDLGSSFFPAAGTIVITTTGFGNISPRTGEGKIFCIIYALLGIPLFGLLAGVDQ 180
DB 121 SNOISHWDLGSSFFPAAGTIVITTTGFGNISPRTGEGKIFCIIYALLGIPLFGLLAGVDQ 180
QY 181 LGTIFGKIAKVEDTIFKNNVSOTKIRIITSTIIFILFGCVLFAALPAIIFKHEGMSALD 240
DB 181 LGTIFGKIAKVEDTIFKNNVSOTKIRIITSTIIFILFGCVLFAALPAIIFKHEGMSALD 240
QY 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVWFMIIVGLAYFAAVLSMIGDMLRVIS 300
DB 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVWFMIIVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEVGEFRAAEMTAVTAEPKETERRLSVELDYKFORATSIKRLSALAGNHQ 360
DB 301 KKTKEVGEFRAAEMTAVTAEPKETERRLSVELDYKFORATSIKRLSALAGNHQ 360
QY 361 ELTPCRRITLVNHLASERDVLPLLTSTESIYNGLTTPHCAGEIAVIENIK 411
DB 361 ELTPCRRITLVNHLASERDVLPLLTSTESIYNGLTTPHCAGEIAVIENIK 411
RESULT 2
QY 08HY88 PRELIMINARY; PRT; 411 AA.
AC 08HY88;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Potassium channel subfamily K member 2.
GN KCNK2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal cortex;
RX PubMed=12368289;
RA Eysaert J.J., Xu L., Danthi S., Eysaert J.A.;
RT "An ACTH- and ATP-regulated Background K+ Channel in Adrenocortical
RT Cells Is TREK-1."
RL J. Biol. Chem. 277:49186-49199(2002).
DR EMBL; AY148474; AAN37591.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:000567; P:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003976; K+channel_pore.
DR PRINTS; PR01333; 2PORKCHANEL.
DR PRINTS; PR01499; TREKCHANEL.
SQ SEQUENCE 411 AA; 45438 MW; A185EAC20A68CCDC CRC64;
Query Match 99.2%; Score 2082; DB 6; Length 411;
Best Local Similarity 99.3%; Pred. No. 5,2e-165;
Matches 408; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINWKMKTGSTIFLVVLYLI 60
DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINWKMKTGSTIFLVVLYLI 60
QY 61 GATVFALQEPHEISORTTIVIOKOTFISQHSQVNSTELDELIOQIVAINAGIIPLCNT 120
DB 61 GATVFALQEPHEISORTTIVIOKOTFISQHSQVNSTELDELIOQIVAINAGIIPLCNT 120

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QY 121 SNOISHWDLGSSFFPAAGTIVITTTGFGNISPRTGEGKIFCIIYALLGIPLFGLLAGVDQ 180
DB 121 SNOISHWDLGSSFFPAAGTIVITTTGFGNISPRTGEGKIFCIIYALLGIPLFGLLAGVDQ 180
QY 181 LGTIFGKIAKVEDTIFKNNVSOTKIRIITSTIIFILFGCVLFAALPAIIFKHEGMSALD 240
DB 181 LGTIFGKIAKVEDTIFKNNVSOTKIRIITSTIIFILFGCVLFAALPAIIFKHEGMSALD 240
QY 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVWFMIIVGLAYFAAVLSMIGDMLRVIS 300
DB 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVWFMIIVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEVGEFRAAEMTAVTAEPKETERRLSVELDYKFORATSIKRLSALAGNHQ 360
DB 301 KKTKEVGEFRAAEMTAVTAEPKETERRLSVELDYKFORATSIKRLSALAGNHQ 360
QY 361 ELTPCRRITLVNHLASERDVLPLLTSTESIYNGLTTPHCAGEIAVIENIK 411
DB 361 ELTPCRRITLVNHLASERDVLPLLTSTESIYNGLTTPHCAGEIAVIENIK 411
RESULT 3
QY 092086 PRELIMINARY; PRT; 426 AA.
AC 092086;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE 2P domain potassium channel KCNK2 (Tandem pore domain potassium
DE channel TREK-1).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21219399; PubMed=11319556;
RA Bockenhauer D., Zilberberg N., Goldstein S.A.;
RT "KCNK2: reversible conversion of a hippocampal potassium leak into a
RT voltage-dependent channel."
RL Nat. Neurosci. 4:486-491(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=21896087; PubMed=11897838;
RA Gu W., Schlichter G., Hirsch J.R., Engels H., Karschin C.,
RA Karschin A., Derst C., Steinlein O.K., Daut J.;
RT "Expression pattern and functional characteristics of two novel splice
RT variants of the two-pore-domain potassium channel TREK-2."
RL J. Physiol. 539:657-668(2002).
DR EMBL; AF325671; AAL01159.1; -.
DR EMBL; AF325402; AAL95708.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:000567; P:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003976; K+channel_pore.
DR PRINTS; PR01333; 2PORKCHANEL.
DR PRINTS; PR01499; TREKCHANEL.
KM Ionic channel; Transmembrane.
SQ SEQUENCE 426 AA; 46912 MW; CACDA05BB935PDBC CRC64;
Query Match 96.7%; Score 2028; DB 11; Length 426;
Best Local Similarity 95.6%; Pred. No. 1.7e-160;
Matches 393; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINWKMKTGSTIFLVVLYLI 60
DB 16 VAAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINWKMKTGSTIFLVVLYLI 75

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QY 61 GATVFKALBOPHEISORTTIVIOKOTFISQHSVNSTELDELIOQIVAINAGITPLCNT 120  
DB 76 GATVFKALBOPHEISORTTIVIOKOTFISQHSVNSTELDELIOQIVAINAGITPLCNT 135  
QY 121 SNOISHMDLSSSFFPAGTIVITTTGFGNISPRTEGKIFCIIYALLGIPPLFGFLAGVGDQ 180  
DB 136 SNOVSHMDLSSSFFPAGTIVITTTGFGNISPRTEGKIFCIIYALLGIPPLFGFLAGVGDQ 195  
QY 181 LGTIFGKGIKAKVEDTIFKNNVSQTKIRIISTIIIFILFGCVLPAVIFKAIIEGMSALD 240  
DB 196 LGTIFGKGIKAKVEDTIFKNNVSQTKIRIISTIIIFILFGCVLPAVIFKAIIEGMSALD 255  
QY 241 AIFVAVITLTITGFGYVAGGSDIEYLDYKPVVWFWIIVGLAYFAAVLSMTGDMLRVYS 300  
DB 256 AIFVAVITLTITGFGYVAGGSDIEYLDYKPVVWFWIIVGLAYFAAVLSMTGDMLRVYS 315  
QY 301 KKTKEVGEFRAHAAEWNTAVTAEFKETRRLSVEIYDKFQATSIRKXLSAELAGNHQ 360  
DB 316 KKTKEVGEFRAHAAEWNTAVTAEFKETRRLSVEIYDKFQATSIRKXLSAELAGNHQ 375  
QY 361 ELTPCGRITSVNHLTSEEDVLPPLTKTESIYNGLTPHAGGEIATVIEK 411  
DB 376 ELTPCGRITSVNHLTSEEDVLPPLTKTESIYNGLTPHAGGEIATVIEK 426

## RESULT 4

Q8BZB0 PRELIMINARY; PRT; 453 AA.  
ID Q8BZB0  
AC Q8BZB0  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)  
DE Potassium channel subfamily K member 10 (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium.  
RT Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK036066; BAC29295.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005267; F:potassium channel activity; IEA.  
DR GO; GO:0006113; P:potassium ion transport; IEA.  
DR InterPro; IPR003280; K+channel\_2pore.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR003976; Trek channel.  
DR PRINTS; PR01333; 2PORECHANNEL.  
DR PRINTS; PR01499; TREKCHANNEL.  
FT NON\_TER 453  
SQ SEQUENCE 453 AA; 49958 MW; F8C5C3FF41E823B0 CRC64;

Query Match 59.5%; Score 1248.5; DB 11; Length 453;  
Best Local Similarity 64.6%; Pred. No. 1.6e-95;  
Matches 244; Conservative 58; Mismatches 65; Indels 11; Gaps 5;

QY 2 AARDLDPKSA--AQNSKRLSTSTKPTVLAASVEDT---TINWKMKTVSTIFLVVL 56  
DB 20 AARDLDPKSA--AQNSKRLSTSTKPTVLAASVEDT---TINWKMKTVSTIFLVVL 78  
QY 57 YLIGATVFKALBOPHEISORTTIVIOKOTFISQHSVNSTELDELIOQIVAINAGITP 116  
DB 79 YLIGATVFKALBOPHEISORTTIVIOKOTFISQHSVNSTELDELIOQIVAINAGITP 138  
QY 117 LGTISNQHMDLSSSFFPAGTIVITTTGFGNISPRTEGKIFCIIYALLGIPPLFGFLAG 176

DB 139 VGNSSNSSHMDLSSSFFPAGTIVITTTGFGNISPRTEGKIFCIIYALLGIPPLFGFLAG 198  
QY 177 VGDOLGTIFGKGIKAKVEDTIFKNNVSQTKIRIISTIIIFILFGCVLPAVIFKAIIEG 236  
DB 199 VGDOLGTIFGKGIKAKVEDTIFKNNVSQTKIRIISTIIIFILFGCVLPAVIFKAIIEG 258  
QY 237 SALDAIFVAVITLTITGFGYVAGG--SDIEYLDYKPVVWFWIIVGLAYFAAVLSMTGDM 295  
DB 259 TALDSITIFVAVITLTITGFGYVAGG--SDIEYLDYKPVVWFWIIVGLAYFAAVLSMTGDM 318  
QY 296 LRVISKKTKEVGEFRAHAAEWNTAVTAEFKETRRLSVEIYDKFQATSIRKXLSAELAG 351  
DB 319 LRVISKKTKEVGEFRAHAAEWNTAVTAEFKETRRLSVEIYDKFQATSIRKXLSAELAG 378  
QY 352 AELAGNHQELTPCGRITL 369  
DB 379 LDRPHSLDMLSPKRSV 396

## RESULT 5

Q8BWL1 PRELIMINARY; PRT; 535 AA.  
ID Q8BWL1  
AC Q8BWL1  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)  
DE Potassium channel subfamily K member 10.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium.  
RT Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK036153; BAC38424.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005267; F:potassium channel activity; IEA.  
DR GO; GO:0006113; P:potassium ion transport; IEA.  
DR InterPro; IPR003280; K+channel\_2pore.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR003976; Trek channel.  
DR PRINTS; PR01333; 2PORECHANNEL.  
DR PRINTS; PR01499; TREKCHANNEL.  
FT NON\_TER 535  
SQ SEQUENCE 535 AA; 59401 MW; 3B98E89F875C26BD CRC64;

Query Match 59.5%; Score 1248.5; DB 11; Length 535;  
Best Local Similarity 64.6%; Pred. No. 2e-95;  
Matches 244; Conservative 58; Mismatches 65; Indels 11; Gaps 5;

QY 2 AARDLDPKSA--AQNSKRLSTSTKPTVLAASVEDT---TINWKMKTVSTIFLVVL 56  
DB 20 AARDLDPKSA--AQNSKRLSTSTKPTVLAASVEDT---TINWKMKTVSTIFLVVL 78  
QY 57 YLIGATVFKALBOPHEISORTTIVIOKOTFISQHSVNSTELDELIOQIVAINAGITP 116  
DB 79 YLIGATVFKALBOPHEISORTTIVIOKOTFISQHSVNSTELDELIOQIVAINAGITP 138  
QY 117 LGTISNQHMDLSSSFFPAGTIVITTTGFGNISPRTEGKIFCIIYALLGIPPLFGFLAG 176  
DB 139 VGNSSNSSHMDLSSSFFPAGTIVITTTGFGNISPRTEGKIFCIIYALLGIPPLFGFLAG 198  
QY 177 VGDOLGTIFGKGIKAKVEDTIFKNNVSQTKIRIISTIIIFILFGCVLPAVIFKAIIEG 236  
DB 199 VGDOLGTIFGKGIKAKVEDTIFKNNVSQTKIRIISTIIIFILFGCVLPAVIFKAIIEG 258  
QY 237 SALDAIFVAVITLTITGFGYVAGG--SDIEYLDYKPVVWFWIIVGLAYFAAVLSMTGDM 295

Db 259 TALESIYFVVVLTITVPGDFVAGNAGINREMYKPLVFWILVGLAVFAVLSMIGDW 316  
 Qy 296 LRVISCKTKEEVEGEPFAHAAEWTANTVAFKTERRLSTVYDKQRTST---KRLIS 351  
 Db 319 LRVISCKTKEEVEGEIYAHAAEKAVNTAFERTRRLSVYEHDKQRAATIRSMERRLG 378  
 Qy 352 AELAGNNQELTFPCRRTL 369  
 Db 379 LDQRAHSLDMLSPKRSV 396

RESULT 6  
 Q92414 PRELIMINARY; PRT; 397 AA.  
 ID Q92414  
 AC Q92414  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Mechanosensitive tandem pore potassium channel.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NC NCBI\_TaxID=10116;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RA MEDLINE=21268449; PubMed=11374070;  
 RA Kim Y., Bang H., Gattencio C., Kim D.;  
 RT "Synergistic interaction and the role of C-terminus in the activation  
 RT of PMAK K+ channels by pressure, free fatty acids and alkali";  
 RL Pflügers Arch. 442:64-72(2001).  
 DR EMBL: AFJ02842; AAK60504.2; -;  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0005216; F:ion channel activity; IEA.  
 DR GO: GO:0005267; F:potassium channel activity; IEA.  
 DR GO: GO:0006813; P:potassium ion transport; IEA.  
 DR InterPro: IPR001980; Granin.  
 DR InterPro: IPR003280; K+channel\_2pore.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR008074; TRAK channel.  
 DR Pfam: PF01271; Granin.1.  
 DR PRINTS: PRO1333; 2PORECHANNEL.  
 DR PRINTS: PRO1691; TRAKCHANNEL.  
 KW Ionic channel.  
 SQ SEQUENCE 397 AA; 42987 MW; 3AF04C43FA982D22 CRC64;

Query Match 36.4%; Score 764.5; DB 11; Length 397;  
 Best Local Similarity 48.8%; Pred. No. 2.9e-55;  
 Matches 139; Conservative 57; Mismatches 86; Indels 3; Gaps 1;  
 Qy 42 MKKKVSTIFLVVLYLIGATVFKALBPHEISQRTTIVIOKQTFISQHSVNSTELDE 101  
 Db 1 MRSSTLLALLVLLVLYLVSGLVFPALBPHEQVQVQKDLBGRDQFLKDPVCSQKNEG 60  
 Qy 102 LIIQIVAAINAGIIP--LGNTSNOISHWDLGSSFFPAGTVTTTIGFNGISPRTEGKIF 158  
 Db 61 FKLVAELGGGANPEISWNTSSNSAANLGSAPFFSGTITTTIGYNALHTDAGRLF 120  
 Qy 159 CIYALALGIPFGFLAGVGDQGITFGKGLAKVDTIKKVNOSTKRIIISTIIIFILFG 218  
 Db 121 CEFYAVVGIPFGMLAGVGRDGLSSLRGIGHIAVFLKMHVPDGLVPMASVAVFLILIG 180  
 Qy 219 CVLFEVALPAIFKEHIGMSALDAIFYVVVLTITVFGDVVAGSGSIEVLDKPKPVWMI 278  
 Db 181 CLFVLTPTFFVSYKMSKKAIFYVLTITVFGDVVPDGDGQNSPVRQPLVWMI 240  
 Qy 279 LVGLAVFAVLSMIGDWLRVISKTKKEVEGEPFAHAAEWTANTVAF 323  
 Db 241 LFGLAFFASVFTTIGNMLRAVSRRTRAEWGGLTAQASMTGTVTA 285

RESULT 7  
 Q9CX88

ID Q9CX88 PRELIMINARY; PRT; 241 AA.

AC Q9CX88  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE 3010005K24Rik protein.  
 GN 3010005K24Rik.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCBI\_TaxID=10090;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TRISUE=Embryo;  
 RA MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Atakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schiraldi L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,  
 RA Blake J., Botelli D., Bojunga N., Carninci P., de Bonaldo K.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Maeshima U., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuka S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK019376; BAB31686.1; -;  
 DR MGD: MGI:1924704; 3010005K24Rik.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0005267; F:potassium channel activity; IEA.  
 DR GO: GO:0006813; P:potassium ion transport; IEA.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR003976; Trek channel.  
 DR PRINTS: PRO1499; TREKCHANNEL.  
 SQ SEQUENCE 241 AA; 25799 MW; B4C39F77CD0A39DA CRC64;

Query Match 29.4%; Score 616; DB 11; Length 241;  
 Best Local Similarity 61.5%; Pred. No. 3.6e-43;  
 Matches 123; Conservative 28; Mismatches 43; Indels 6; Gaps 3;  
 Qy 2 AADPLDPSXA--AONSKPRLSPSTKPTVLAASVSDT---TINWKKWTVSTIFLVVYL 56  
 Db 23 AAPVCPKPSATNGHHHPVRLSSRAIVYA-RMEASGGGQITWKKWTVVAFVWVYV 81  
 Qy 57 YLIIGATVFKALBPHEISQRTTIVIOKQTFISQHSVNSTELDLIIQIVAAINAGIIP 116  
 Db 82 YLVTGGLVFPALBPHESSQKNTIALEKAEFRDHCVPQPELTLIQALADNAGVSP 141  
 Qy 117 LGNTSNOISHWDLGSSFFPAGTVTTTIGFNGISPRTEGKICIIYALGIPFGILAG 176  
 Db 142 VGNSSNSSSHWDGSAFFPAGTVTTTIGYNALPSTGGKIFCLYALGIPFGILAG 201  
 Qy 177 VGDQGTIFGKGLAKVEDTF 196  
 Db 202 IGDQGTIFGKGLAKVEDTF 221

RESULT 8  
 ID Q9UK62 PRELIMINARY; PRT; 502 AA.  
 AC Q9UK62;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Potassium channel TASK2 (TASK2 potassium channel).  
GN KCNK5.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/Svj; TISSUE=Kidney;  
RA Roux J., Barhanin J.,  
RT "Mouse two P domain potassium channel TASK2.";  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Cid L.P., Niemeyer M.I., Sepulveda F.V.;  
RT "Functional properties of mouse TASK-2 potassium channel.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Kidney;  
RX MEDLINE=2354683; Pubmed=1246851;  
RA The FANTOM Consortium.  
RT "The Riken Genome Exploration Research Group Phase I & II Team."  
RL "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RT Nature 420:563-573(2002).  
DR EMBL; AF259395; AAF68668.1; -;  
DR EMBL; AF259395; AAF68668.1; -;  
DR EMBL; AF259395; AAF68668.1; -;  
DR EMBL; AF259395; AAF68668.1; -;  
DR MGD; MGI:1336175; Kcnk5.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005216; F:ion channel activity; IEA.  
DR GO; GO:0005267; F:potassium channel activity; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR InterPro; IPR003280; K+channel\_2pore.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR003092; TASK\_channel.  
DR PRINTS; PRO1333; 2PORECHANNEL.  
DR PRINTS; PRO1095; TASKCHANNEL.  
DR KX ionic channel.  
SQ SEQUENCE 502 AA; 55976 MW; E4C7E7C71B44D95 CRC64;  
Query Match 19.8%; Score 415; DB 11; Length 502;  
Best Local Similarity 30.5%; Pred. No. 5.1e-26;  
Matches 104; Conservative 63; Mismatches 120; Indels 54; Gaps 11;  
QY 54 VVLLIIGATVFALBQPHISORTIIVIQKOTFISQHSQVNSTELDEHIIQIVAINAG 113  
DB 12 IIFYLAIGALFEVLEBPHKEAKKNYYQKHLMEFCLSGEGDKILQVVSADAG 71  
QY 114 IIFLGNTSNOISHWDLGSSFFPAGTYITTTGFGNISPRTEGGKIPCTITALLGIPFGFL 173  
DB 72 VAITGQGT--FNWNNPNAWIFAAVITTTIGYGVAPKTPAGRLFCVFYGLFGEVPL---C 126  
QY 174 IAGVGDQLGTIFGKGIKAVEDTFIKMNVSTKIRIISTIFILFGCVLFAALPAIFKHI 233  
DB 127 LTVI-SALGKFFGGRARLGOPLTRGVSLRKAQITCTAIFIVGVLVAVLPPFVFWT 185  
QY 234 EGSALDAIFYVITTTTIGFDYVAG-GSDIYLDIFYKVVFWLVLGLVFAVLSMI 292  
DB 186 EEWNYIEGLYISFTITSTIGFDVAGVNSANYHALYRFVFLWITVLGLAW---LSIF 241  
QY 293 GDMRVISKTKREVGCFRAHAEMNANYAEKRETRRSVSIYKPKRASIKKLSA 352  
DB 242 VNN-----KVSNF-----VYHKAIKKRRR-----RKESF 267  
QY 353 ELAGNNQELTPCRRLSVNHLTSESDV--LPPLLTESIY 391  
DB 268 E-SSPHS-----RKALQWAGSTASKDVNIFSLSKKEEY 301

08H272 ID ID PRELIMINARY; PRT; 341 AA.  
AC 08H272.  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Potassium channel TASK-4.  
GN KCNK17.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Derst C., Reignta V.K., Preisig-Mueller R., Rajan S., Daut J.;  
RT "Cloning and sequencing of bovine potassium channel TASK-4.";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF479760; AAN2894.1; -;  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005267; F:potassium channel activity; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR InterPro; IPR003280; K+channel\_2pore.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR003092; TASK\_channel.  
DR PRINTS; PRO1333; 2PORECHANNEL.  
DR PRINTS; PRO1095; TASKCHANNEL.  
SQ SEQUENCE 341 AA; 37695 MW; 0A21FEA71B39401 CRC64;  
Query Match 19.7%; Score 413; DB 6; Length 341;  
Best Local Similarity 37.2%; Pred. No. 4.5e-26;  
Matches 93; Conservative 53; Mismatches 92; Indels 12; Gaps 6;  
QY 48 STIFLV--VVYLLIGATVFALBQ--HEISQRTIIVIQKOTFISQHSQVNSTELDEHII 103  
DB 35 STLLLLLYLVLYLVIGTCVFWALSSPAHDSKR--FGQDKWALLRNPTCLDGGALDSLI 92  
QY 104 QQIVAAINAGIIFLGNTSNOISHWDLGSSFFPAGTYITTTGFGNISPRTEGGKIPCTI 163  
DB 93 RGIIEAYNGDIVGNTTS--NGRWEFVGSFFSVSTITTTIGYGLSPRTMAARLFCIFFA 151  
QY 164 ILGIFLFGFLLAGVGDQLGTIFGKGIKAVEDTFIKMNVSTKIRIISTIFILFGCVL 223  
DB 152 LVGIFPLNIVL---NRLGHCMQGVHRCARLGAANKDPKAKWLAGSSLLIGLLFL 207  
QY 224 ALPAIFHIGWSDALDAIFYVITTTTIGFDYVAG-GSDIYLDIFYKVVFWLVLGL 282  
DB 208 LLPPLLFHNMGMWTVGEGFYSFVTLSTVGFDVAVIGNPSERNPLWYQNTSLMILFGM 267  
QY 283 AYFAVLSMI 292  
DB 268 AMLALITKLI 277  
RESULT 10  
080XEO ID ID PRELIMINARY; PRT; 257 AA.  
AC 080XEO.  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Similar to potassium channel, subfamily K, member 5 (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RA Strausberg R.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC051088; AAH51088.1;  
DR GO; GO:0016020; C:membrane; IEA.

DR GO: GO:0005216; F-1 ion channel activity; IEA.  
DR GO: GO:0005267; F-1 potassium channel activity; IEA.  
DR GO: GO:0006813; P-1 potassium ion transport; IEA.  
DR InterPro: IPR003280; K+channel\_2pore.  
DR InterPro: IPR001622; K+channel\_pore.  
DR InterPro: IPR003093; TASK\_channel.  
DR PRINTS; PR01333; 2PORKCHANNEL.  
DR PRINTS; PR01095; TASKCHANNEL.  
DR KW Ionic channel.  
FT NON TER 257 257  
SQ SEQUENCE 257 AA; 29001 MW; AA00FB04152126C4 CRC64;

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 19.5%            | Score 409.5;       | DB 11;     | Length 257; |
| Best Local Similarity | 34.2%;           | Pred. No. 6.2e-26; |            |             |
| Matches 83;           | Conservative 55; | Mismatches 94;     | Indels 11; | Gaps 5;     |

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OY      5  VWYLLIIGAVFKALEOPIEISQRTTIVIOKOTFISOSHCSVNSTEDELIQQVAINNG  113
Db      12  IIFYLLIIGAAIFVELEPPEMKRAKNVYTQCLHLKXEPCLCSGEGDKXILQVSDAADG  71
OY      114 IIPLGNTSQIASHMDIGSEFFPAGVITTTIGFNGISPTBGGKICETIYALGIPLEGFL  173
Db      72  VAITGQOT--FNNMWNPNMIFMAATVITTTIGYGVAAKTPAGRIFCVYGLFSGVP---C  126
OY      174 LAQVGNQLGTFPGKIAKVEDTFIFIMWNSQKIRIISITFIPLFGCVLPAALPAIFKHII  233
Db      127  LTMF-SALGKFRGGRAKKLGQFLTRGVSLSKKAQITCTALFIYWGVLVHLVIPPEFMYT  185
OY      234 EGNSSALDAIYFVVIITTTIGFGDYVAG-GSDIEYLFYKPYVMFWIIVGLAYFAVALSMI  292
Db      186  EENNYIEGIIYSEITITSTIGFGDFVAGVNPANTHALYRFVEIIMIVLGLAW----LSLF  241
OY      293  GDM  295
Db      242  VNM  244

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| RESULT | 11  |
|--------|---|
| 0801T4 |   |
| ID     | PRELIMINARY; PRT; 307 AA.   |
| AC     | 0801T4;   |
| DT     | 01-JUN-2003 (TREMBLrel. 24, Created)                              |
| DT     | 01-JUN-2003 (TREMBLrel. 24, Last sequence update)                 |
| DT     | 01-OCT-2003 (TREMBLrel. 25, Last annotation update)               |
| DE     | Similar to potassium channel, subfamily K, member 6 (TWIK-2).     |
| OS     | Xenopus laevis (African clawed frog).                             |
| OC     | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC     | Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;     |
| CC     | Xenopodinae; Xenopus.   |
| OX     | NCBI_taxid=8355;  |
| RN     | [1]   |
| RP     | SEQUENCE FROM N.A.  |
| RC     | TISSUE=Embryo;  |
| RA     | Klein S., Strausberg R.;  |
| RL     | Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.           |
| EMBL   | BC047247; AAH47247.1; ..  |
| DR     | GO: GO:0016021; C:integral to membrane; IEA.                      |
| DR     | GO: GO:0005216; F:ion channel activity; IEA.                      |
| DR     | GO: GO:0005267; F:potassium channel activity; IEA.                |
| DR     | GO: GO:0006811; P:ion transport; IEA.                             |
| DR     | GO: GO:0006813; P:potassium ion transport; IEA.                   |
| DR     | InterPro: IPR005821; Ion trans                                    |
| DR     | InterPro: IPR003280; K+Channel 2pore.                             |
| DR     | InterPro: IPR001622; K+Channel pore.                              |
| DR     | InterPro: IPR001779; TWIK1_Channel.                               |
| DR     | InterPro: IPR005408; TWIK_Channel.                                |
| DR     | Pfam: PF00520; Ion trans; 1.                                      |
| DR     | PRINTS: PRO1333; 2FORECHANNEL.                                    |
| DR     | PRINTS: PRO1096; TWIK1CHANNEL.                                    |
| DR     | PRINTS: PRO1566; TWIKCHANNEL.                                     |
| DR     | IONIC channel.  |
| QO     | SEQUENCE 307 AA; 35190 MW; E7C48BB553B94BE9 CRC64;                |

[illegible]

| RESULT 12 | QSN4VS  | PRELIMINARY; | PRT; | 184 AA. |
|-----------|---|--------------|------|---------|
| ID        | QSN4VS  |              |      |         |
| AC        | QSN4VS;   |              |      |         |
| DT        | 01-OCT-2002 (TREMBLrel. 22, Created)                              |              |      |         |
| DT        | 01-OCT-2002 (TREMBLrel. 22, Last sequence update)                 |              |      |         |
| DT        | 01-JUN-2003 (TREMBLrel. 24, Last annotation update)               |              |      |         |
| DE        | Similar to potassium channel, subfamily X, member 4.              |              |      |         |
| OS        | Homo sapiens (Human).   |              |      |         |
| OC        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |              |      |         |
| OC        | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.         |              |      |         |
| OX        | NCBI_TaxID=9606;  |              |      |         |
| RN        | [1]   |              |      |         |
| RP        | SEQUENCE FROM N.A.  |              |      |         |
| RC        | TISSUE=Brain;   |              |      |         |
| RA        | Strausberg R.;  |              |      |         |
| RL        | Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.           |              |      |         |
| DR        | EMBL; BC033577; AAH33577.1; -.                                    |              |      |         |
| DR        | GO; GO:0016020; C:membrane; IEA.                                  |              |      |         |
| DR        | GO; GO:0005216; F:ion channel activity; IEA.                      |              |      |         |
| DR        | GO; GO:0005267; F:potassium channel activity; IEA.                |              |      |         |
| DR        | GO; GO:0006813; P:potassium ion transport; IEA.                   |              |      |         |
| DR        | InterPro; IPR001622; K+channel pore.                              |              |      |         |
| DR        | InterPro; IPR003976; Trek channel.                                |              |      |         |
| DR        | PRINTS; PR01499; TREKCHANNEL.                                     |              |      |         |
| DR        | Ionic channel.  |              |      |         |
| QO        | SEQUENCE 184 AA; 19380 MW; A96A6B586D40AF60 CRC64;                |              |      |         |

|           |                       |   |              |           |                                  |
|-----------|-----------------------|---|--------------|-----------|----------------------------------|
|           | Query Match           | 19.1%   | Score 400;   | DB 4;     | Length 184;                      |
|           | Best Local Similarity | 48.1%;  | Pred. No.    | 2, 56-25; |                                  |
|           | Matches               | 76;   | Conservative | 34;       | Mismatches 46; Indels 2; Gaps 1; |
| Qy        | 42                    | MKAKTVSTILVNVYLIITGATVPKALCEPHEHSQRTTIVIQQTISCHSCYNSELDL      | 101          |           |                                  |
| Db        | 27                    | MRSTTLIALVALVLVSGALFPALECPHEEQADPEGEVEKEFLRAFPVSDDELGL        | 86           |           |                                  |
| Qy        | 102                   | LIDQIVAIAINAGIIPLENTSNOQISH--WDLGSSPFAPGIYTTIGFNISPRTEGGKIFPC | 159          |           |                                  |
| Db        | 87                    | LIREVDALGGADPETNSTSNSSHSMWDGSAFFESGITIIITIGYNVALRTDAGRLLFC    | 146          |           |                                  |
| Qy        | 160                   | IYAALLGIPLEGFLLAGVPDLGTTFPGKGIAKYEDPTI                        | 197          |           |                                  |
| Db        | 147                   | IFYALVGIPLEGILLAGVDRLLGSSLRHGICHTAEAFLL                       | 184          |           |                                  |
| RESULT 13 |                       |   |              |           |                                  |
| Q8R454    | ID                    | PRELIMINARY;  | PRT;         | 336 AA.   |                                  |

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AC      08R454.2002 (Tremblrel. 21, Created)
DT      01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT      01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE      Potassium channel TWIK-1.
GN      KCNK1.
OS      Cavia porcellus (Guinea pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
CX      NCBI_taxid=10141;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Derst C., Rajan S., Preisig-Mueller R.;
RT      "Cloning and sequencing of guinea pig TWIK channels."
RL      Submitted (JAN-2002) to the EMBL/GenBank/DDBB databases.
RR      EMBL; AY075096; AAL82795.1; -.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0005216; F:ion channel activity; IEA.
DR      GO; GO:0005267; F:potassium channel activity; IEA.
DR      GO; GO:0006813; P:potassium ion transport; IEA.
DR      InterPro; IPR003280; K-channel_2pore.
DR      InterPro; IPR001622; K-channel_pore.
DR      InterPro; IPR001779; TWIK_channel.
DR      InterPro; IPR005408; TWIK_channel.
DR      PRINTS; PR01333; 2PORECHANNEL.
DR      PRINTS; PR01096; TWIK1CHANNEL.
DR      PRINTS; PR01586; TWIKCHANNEL.
DR      Ionc channel; Transmembrane.
SQ      SEQUENCE 336 AA, 38102 MW, 299B6915907FF5B2A CRC64;

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|                       |        |                    |        |                 |
|-----------------------|--------|--------------------|--------|-----------------|
| Query Match           | 18.1%; | Score 380;         | DB 11; | Length 336;     |
| Best Local Similarity | 30.0%; | Pred. No. 2.5e-23; |        |                 |
| Matches               | 92;    | Conservative       | 69;    | Mismatches 120; |
|                       |        |                    | Indels | 26;             |
|                       |        |                    | Gaps   | 9               |

[illegible]

|    |     |         |     |
|----|-----|---------|-----|
| QY | 330 | RRLSVEI | 336 |
|    |     | ::: ::: |     |
| Db | 320 | PFVAAQV | 326 |

|              |         |
|--------------|---------|
| RESULT 14    |         |
| Q922T2       |         |
| ID Q922T2    |         |
| PRELIMINARY; |         |
| PRT;         | 336 AA. |

AC Q92412;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)  
DE Putative potassium channel TWIK.  
OS *Rattus norvegicus* (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]\_\_\_\_\_  
RP SEQUENCE FROM N.A.

PA Gan L., Poliner W.T., Quinn A.M., Wang L.-Y., Hughes T.,  
RA Kuzmarek L.K.,  
RT "Cloning and localization of rTWIK, a putative potassium channel with  
RT two P domains".  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF022819; AAD09336.1; -.  
DR GC: GO:0016031; C:integral to membrane; IEA.  
DR GC: GO:0005216; F:ion channel activity; IEA.  
DR GO: GO:0005267; F:potassium channel activity; IEA.  
DR GO: GO:0006813; P:potassium ion transport; IEA.  
DR InterPro: IPR001280; K+channel\_3Dore.  
DR InterPro: IPR001623; K+channel\_3Dore.  
DR InterPro: IPR001776; TWIK\_channel.  
DR InterPro: IPR005408; TWIK\_channel.  
DR PRINTS: PRO1333; ZPFOREKCHANEL.  
DR PRINTS: PRO1096; TWIK1CHANNEL.  
DR PRINTS: PRO1586; TWIK1CHANNEL.  
DR Ionic\_channel; Transmembrane.  
KW SEQUENCE 336 AA; 38228 MW; SE78031947D75DE6 CRC64;

|                       |        |                    |        |                 |
|-----------------------|--------|--------------------|--------|-----------------|
| Query Match           | 18.0%; | Score 378.5;       | DB 11, | Length 336;     |
| Best Local Similarity | 32.5%; | Pred. No. 3.3e-23; |        |                 |
| Matches               | 90;    | Conservative       | 62;    | Mismatches 108; |
|                       |        |                    | Indels | 17;             |
|                       |        |                    | Gaps   | 9;              |

```

QY      51  ILVVV--VMIILIGATVKALEQPHIEIORITIVIQKQTFISQHSQVNSTEIDELIQOIVA 108
      25  FLVIGVLLYLVFVGWVSVSELPEDILLROELRKLKRFLESHCELSBPQJQGLSKVLE  84
Dh
QY      109  AINAGIIPLGNTSNOISHMDLGSSFPFAGVITTTIGFNTSPRTGGKIFCITIALLGIP 168
      85  ASNVGAVLSNAGSN--NMWDEFTSLPFASTVLSITTGHTVPLSDGKAFCIIVSVIGIP 143
Dh
QY      169  LFGVLGAVGDQLOITIRFGKIAKVEDFIKMNVSQCTIRIISTLI--FILEGCVLFAVLP 226
      144  FTLLFLFAVVOQVAVVAVTR--RPLVLYHIRKGSQOVAAIHAVALIGFVIVSCFFTI--P 193
Dh
QY      227  AIIKPIIE--GMSALDAIYFVITVITTTIGFGDYVAG--GSDIEYLDYFVPMFIMLVGAY 284
      200  AAVPSVLEDDMNFLESEFYCFRISTIGLGDYVGEQGNQKRFRELYKIGITCYLLGLIA 259
Dh
QY      285  FAATVLSMIGDMLRYISK-----KKKEVGEFRRAHAAE 316
Dh      260  MLVAVLETFCF--LHELKPRKRYFYVKKQKQDEQVHIME 295

```

RESULT 15  
999L99  
Q99L99  
PRELIMINARY;  
PRT; 336 AA.

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DT 02-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE Potassium channel, subfamily Kv member 1.
GN KCNK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003729; AA03729.1; -.
DR WGB; M61109322; KCNK1.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005216; F:Ion channel activity; IEA.
DR GO; GO:0005267; F:Potassium channel activity; IEA.
DR GO; GO:0006813; P:Potassium ion transport; IEA.
DR InterPro; IPR003280; K-channel_pore.
DR InterPro; IPR001622; K-channel.
DR InterPro; IPR001779; TWIK_channel.
DR InterPro; IPR005408; TWIK_channel.
DR PRINTS; PR01333; 2PORKCHANNEL.

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2004, 17:58:38 ; Search time 46 Seconds  
(without alignments)  
2792.661 Million cell updates/sec

Title: US-09-980-350-2

Sequence: 1 MAAPDLIDPKSAQAQNSKPRLL.....LNGLTPHCAGEIAVLENIK 411

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

1285345 segs, 312560633 residues

Total number of hits satisfying chosen parameters: 1285345

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubppaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppaa/US10C\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubppaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description       |
|------------|--------|-------------|--------|----|-------------------|
| 1          | 2098   | 100.0       | 411    | 9  | US-09-828-746-2   |
| 2          | 2098   | 100.0       | 411    | 14 | US-10-121-746-83  |
| 3          | 2095   | 99.9        | 411    | 12 | US-09-892-360-18  |
| 4          | 2065   | 98.4        | 426    | 8  | US-08-816-011-45  |
| 5          | 2038   | 97.1        | 411    | 9  | US-09-828-746-6   |
| 6          | 1824   | 86.9        | 370    | 9  | US-09-939-484-8   |
| 7          | 1824   | 86.9        | 370    | 9  | US-09-939-483-8   |
| 8          | 1248.5 | 59.5        | 538    | 9  | US-09-729-920-5   |
| 9          | 1242.5 | 59.2        | 526    | 9  | US-09-729-920-4   |
| 10         | 1242.5 | 59.2        | 538    | 12 | US-09-892-360-2   |
| 11         | 1242.5 | 59.2        | 543    | 9  | US-09-729-920-2   |
| 12         | 1242.5 | 59.2        | 543    | 12 | US-10-262-511-106 |
| 13         | 1242.5 | 59.2        | 543    | 12 | US-09-852-386-73  |
| 14         | 1242.5 | 59.2        | 543    | 14 | US-10-332-175-2   |
| 15         | 1215   | 57.9        | 724    | 12 | US-10-332-447-10  |

|    |       |      |      |    |                    |                   |
|----|-------|------|------|----|--------------------|-------------------|
| 16 | 803   | 38.3 | 392  | 9  | US-09-747-835A-55  | Sequence 55, Appl |
| 17 | 803   | 38.3 | 392  | 12 | US-10-312-812-55   | Sequence 55, Appl |
| 18 | 803   | 38.3 | 393  | 14 | US-10-243-033-2    | Sequence 2, Appl  |
| 19 | 803   | 38.3 | 419  | 9  | US-09-828-035-2    | Sequence 2, Appl  |
| 20 | 803   | 38.3 | 419  | 14 | US-10-345-680-44   | Sequence 44, Appl |
| 21 | 803   | 38.3 | 419  | 14 | US-10-146-733-29   | Sequence 29, Appl |
| 22 | 803   | 38.3 | 419  | 15 | US-10-352-684A-8   | Sequence 8, Appl  |
| 23 | 803   | 38.3 | 419  | 15 | US-10-391-399-19   | Sequence 19, Appl |
| 24 | 803   | 38.3 | 1314 | 9  | US-09-747-835A-29  | Sequence 29, Appl |
| 25 | 803   | 38.3 | 1314 | 12 | US-10-312-812-29   | Sequence 29, Appl |
| 26 | 776.5 | 37.0 | 398  | 12 | US-09-892-360-18   | Sequence 18, Appl |
| 27 | 578.5 | 27.6 | 421  | 12 | US-10-276-774-2599 | Sequence 2599, Ap |
| 28 | 547   | 26.1 | 107  | 9  | US-09-828-746-4    | Sequence 4, Appl  |
| 29 | 502.5 | 24.0 | 294  | 12 | US-10-451-892-2    | Sequence 2, Appl  |
| 30 | 502.5 | 24.0 | 294  | 12 | US-10-459-190-2    | Sequence 2, Appl  |
| 31 | 502.5 | 24.0 | 294  | 12 | US-10-459-190-9    | Sequence 9, Appl  |
| 32 | 502.5 | 24.0 | 294  | 13 | US-10-121-866-2    | Sequence 2, Appl  |
| 33 | 502.5 | 24.0 | 309  | 15 | US-10-080-334-172  | Sequence 172, App |
| 34 | 502.5 | 24.0 | 309  | 15 | US-10-080-334-177  | Sequence 177, App |
| 35 | 501.5 | 23.9 | 239  | 12 | US-10-459-190-11   | Sequence 11, Appl |
| 36 | 498.5 | 23.8 | 292  | 12 | US-10-451-892-6    | Sequence 6, Appl  |
| 37 | 498.5 | 23.8 | 292  | 12 | US-10-451-892-10   | Sequence 10, Appl |
| 38 | 498.5 | 23.8 | 292  | 12 | US-10-459-190-4    | Sequence 4, Appl  |
| 39 | 475.5 | 22.7 | 294  | 12 | US-10-459-190-10   | Sequence 10, Appl |
| 40 | 430   | 20.5 | 499  | 9  | US-09-735-169A-2   | Sequence 2, Appl  |
| 41 | 430   | 20.5 | 499  | 9  | US-09-735-171A-2   | Sequence 2, Appl  |
| 42 | 430   | 20.5 | 499  | 12 | US-10-701-013-2    | Sequence 2, Appl  |
| 43 | 413.5 | 19.7 | 239  | 12 | US-10-459-190-13   | Sequence 13, Appl |
| 44 | 395   | 18.8 | 293  | 12 | US-10-243-552-405  | Sequence 405, App |
| 45 | 393   | 18.7 | 332  | 12 | US-10-332-447-1    | Sequence 1, Appl  |

## ALIGNMENTS

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | MAAPDLIDPKSAQAQNSKPRLLSTPTVLAASVESDTTINVKKKTGTFITLVVLYLI  | 60  |
| DB | 1   | MAAPDLIDPKSAQAQNSKPRLLSTPTVLAASVESDTTINVKKKTGTFITLVVLYLI  | 60  |
| QY | 61  | GATVFALDEPHEISORTTIVQKOTFISOHCNVSTELDELIOOVAINAGTIPLNT    | 120 |
| DB | 61  | GATVFALDEPHEISORTTIVQKOTFISOHCNVSTELDELIOOVAINAGTIPLNT    | 120 |
| QY | 121 | SNOISHMDLGSFFPAGVITTTIGFONISPRTEGKIFCTIYALLGIFPLFGLAGVGDQ | 180 |

US-09-828-746-2

Sequence 2, Application US/09828746

Patent No. US20020028485A1

GENERAL INFORMATION:

APPLICANT: Helen Jane Meadows

APPLICANT: Conrad Gerald Chapman

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GP-30031-D1

CURRENT APPLICATION NUMBER: US/09/828,746

CURRENT FILING DATE: 2001-04-09

PRIOR APPLICATION NUMBER: US 09/236,080

PRIOR FILING DATE: 1999-01-25

PRIOR APPLICATION NUMBER: EP 98300570.3

PRIOR FILING DATE: 1998-01-27

PRIOR APPLICATION NUMBER: UK 9822135.1

PRIOR FILING DATE: 1998-10-09

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 411

TYPE: PRT

ORGANISM: HOMO SAPIENS

US-09-828-746-2

Query Match 100.0%; Score 2098; DB 9; Length 411;

Best Local Similarity 100.0%; Pred. No. 2.4e-197;

Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Db 121 SNOISHWDLGSSFFFACTVITTTIGFNGISPRTEGKIFCIIYALLGLPLFGFLAGVGDQ 180
Qy 181 LGTIFGKIAKVEDTFTKKNVSQTKRIISTITIFILFGCVLPALPAIIFKHIEGMSALD 240
Db 181 LGTIFGKIAKVEDTFTKKNVSQTKRIISTITIFILFGCVLPALPAIIFKHIEGMSALD 240
Qy 241 AIFYVVTITLTITIGFGDYVAGSDIEYDFFKPVVEMIIYGLAYFAAVLSMIGDWLRVIS 300
Db 241 AIFYVVTITLTITIGFGDYVAGSDIEYDFFKPVVEMIIYGLAYFAAVLSMIGDWLRVIS 300
Qy 301 KKTKEEVEGFRPAAAEWNTAVTAIEFKETRRLSVEIYDKFORATSIRKLSAELAGNHNQ 360
Db 301 KKTKEEVEGFRPAAAEWNTAVTAIEFKETRRLSVEIYDKFORATSIRKLSAELAGNHNQ 360
Qy 361 ELTPCRRRLSVNHLTSEKRDVLPPLTKTESIYLNGLPHCAGEBIAYIENIK 411
Db 361 ELTPCRRRLSVNHLTSEKRDVLPPLTKTESIYLNGLPHCAGEBIAYIENIK 411

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# RESULT 2

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US-10-121-746-83
; Sequence 83, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1e1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
; US-10-121-746-83

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Query Match 100.0%; Score 2098; DB 14; Length 411;
Best Local Similarity 100.0%; Pred. No. 2,4e-197;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTVSTIFLVVLYLI 60
Db 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTVSTIFLVVLYLI 60
Qy 61 GATVFALBOPHEISQRTTIVIOKQTFISQSCVNSTEDELIOQIVAAINAGIPLNGT 120
Db 61 GATVFALBOPHEISQRTTIVIOKQTFISQSCVNSTEDELIOQIVAAINAGIPLNGT 120
Qy 121 SNOISHWDLGSSFFFACTVITTTIGFNGISPRTEGKIFCIIYALLGLPLFGFLAGVGDQ 180
Db 121 SNOISHWDLGSSFFFACTVITTTIGFNGISPRTEGKIFCIIYALLGLPLFGFLAGVGDQ 180
Qy 181 LGTIFGKIAKVEDTFTKKNVSQTKRIISTITIFILFGCVLPALPAIIFKHIEGMSALD 240
Db 181 LGTIFGKIAKVEDTFTKKNVSQTKRIISTITIFILFGCVLPALPAIIFKHIEGMSALD 240
Qy 241 AIFYVVTITLTITIGFGDYVAGSDIEYDFFKPVVEMIIYGLAYFAAVLSMIGDWLRVIS 300
Db 241 AIFYVVTITLTITIGFGDYVAGSDIEYDFFKPVVEMIIYGLAYFAAVLSMIGDWLRVIS 300

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Qy 301 KKTKEEVEGFRPAAAEWNTAVTAIEFKETRRLSVEIYDKFORATSIRKLSAELAGNHNQ 360
Db 301 KKTKEEVEGFRPAAAEWNTAVTAIEFKETRRLSVEIYDKFORATSIRKLSAELAGNHNQ 360
Qy 361 ELTPCRRRLSVNHLTSEKRDVLPPLTKTESIYLNGLPHCAGEBIAYIENIK 411
Db 361 ELTPCRRRLSVNHLTSEKRDVLPPLTKTESIYLNGLPHCAGEBIAYIENIK 411

```

# RESULT 3

```

US-09-892-360-18
; Sequence 18, Application US/09892360
; Publication No. US20040101833A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: ROMBEY, GEORGES
; TITLE OF INVENTION: HUMAN TRK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALANTIONAL ANESTHETICS AND
; FILE REFERENCE: 1256-R-00
; CURRENT APPLICATION NUMBER: US/09/892,360
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 60/214,559
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-892-360-18

```

```

Query Match 99.9%; Score 2095; DB 12; Length 411;
Best Local Similarity 99.8%; Pred. No. 4,8e-197;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTVSTIFLVVLYLI 60
Db 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTVSTIFLVVLYLI 60
Qy 61 GATVFALBOPHEISQRTTIVIOKQTFISQSCVNSTEDELIOQIVAAINAGIPLNGT 120
Db 61 GATVFALBOPHEISQRTTIVIOKQTFISQSCVNSTEDELIOQIVAAINAGIPLNGT 120
Qy 121 SNOISHWDLGSSFFFACTVITTTIGFNGISPRTEGKIFCIIYALLGLPLFGFLAGVGDQ 180
Db 121 SNOISHWDLGSSFFFACTVITTTIGFNGISPRTEGKIFCIIYALLGLPLFGFLAGVGDQ 180
Qy 181 LGTIFGKIAKVEDTFTKKNVSQTKRIISTITIFILFGCVLPALPAIIFKHIEGMSALD 240
Db 181 LGTIFGKIAKVEDTFTKKNVSQTKRIISTITIFILFGCVLPALPAIIFKHIEGMSALD 240
Qy 241 AIFYVVTITLTITIGFGDYVAGSDIEYDFFKPVVEMIIYGLAYFAAVLSMIGDWLRVIS 300
Db 241 AIFYVVTITLTITIGFGDYVAGSDIEYDFFKPVVEMIIYGLAYFAAVLSMIGDWLRVIS 300
Qy 301 KKTKEEVEGFRPAAAEWNTAVTAIEFKETRRLSVEIYDKFORATSIRKLSAELAGNHNQ 360
Db 301 KKTKEEVEGFRPAAAEWNTAVTAIEFKETRRLSVEIYDKFORATSIRKLSAELAGNHNQ 360
Qy 361 ELTPCRRRLSVNHLTSEKRDVLPPLTKTESIYLNGLPHCAGEBIAYIENIK 411
Db 361 ELTPCRRRLSVNHLTSEKRDVLPPLTKTESIYLNGLPHCAGEBIAYIENIK 411

```

# RESULT 4

```

US-08-816-011-45
; Sequence 45, Application US/08816011
; Publication No. US20030165806A1
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.

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; APPLICANT: Pausch, Mark H.
; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
; TITLE OF INVENTION: Encoding Them, and Methods of Using Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,011
; FILING DATE: 11-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthews, Gale F.
; REGISTRATION NUMBER: 32,269
; REFERENCE/DOCKET NUMBER: 32,421-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2134
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-816-011-45

```

Query Match 98.4%; Score 2065; DB 8; Length 426;

Best Local Similarity 98.8%; Pred. No. 4,5e-194;

Matches 406; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAONSKRSLFSKPTVLASRVESDITINVMKKTSTIFLVVLYLI 60
DB 16 VAAPDLDPKSAONSKRSLFSKPTVLASRVESDITINVMKKTSTIFLVVLYLI 75
QY 61 GATFKALEOPHEISQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAINAGIIPLGNT 120
DB 76 GATFKALEOPHEISQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAINAGIIPLGNT 135
QY 121 SNOISHWDLGSSFFPAGVITTTIGFNGISPRTEGKIFCIITIALGIFLPGFLLAGVGDQ 180
DB 136 SNOISHWDLGSSFFPAGVITTTIGFNGISPRTEGKIFCIITIALGIFLPGFLLAGVGDQ 195
QY 181 LGTFGKGIKAKVEDFFIKMNSQTKIRIISTIFILFGCVLFAVLPALIPKHIEGMSALD 240
DB 196 LGTFGKGIKAKVEDFFIKMNSQTKIRIISTIFILFGCVLFAVLPALIPKHIEGMSALD 255
QY 241 AIYFVVTITLTIGFGDYVAGSDIEYLDFFKPVVWFILVGLAYFAAVALSMIGWLRLVIS 300
DB 256 AIYFVVTITLTIGFGDYVAGSDIEYLDFFKPVVWFILVGLAYFAAVALSMIGWLRLVIS 315
QY 301 KKTKEVEGFRAHAEMTANTATAEFKETRRLSVEIYDKFORATSIRKLSAELAGNHQ 360
DB 316 KKTKEVEGFRAHAEMTANTATAEFKETRRLSVEIYDKFORATSIRKLSAELAGNHQ 375
QY 361 ELTPCRRITLNVHLTSEEDVLPPLLKTESIYINGLTPHACGEIYAVIENIK 411
DB 376 ELTPCRRITLNVHLTSEEDVLPPLLKTESIYINGLTPHACGEIYAVIENIK 426

```

RESULT 5  
US-09-828-746-6  
; Sequence 6, Application US/09828746  
; Patent No. US20020028485A1  
; GENERAL INFORMATION:

```

; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
;
US-09-828-746-6

```

Query Match 97.1%; Score 2038; DB 9; Length 411;

Best Local Similarity 96.1%; Pred. No. 1,9e-191;

Matches 395; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

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QY 1 MAAPDLDPKSAONSKRSLFSKPTVLASRVESDITINVMKKTSTIFLVVLYLI 60
DB 1 MAAPDLDPKSAONSKRSLFSKPTVLASRVESDITINVMKKTSTIFLVVLYLI 60
QY 61 GATFKALEOPHEISQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAINAGIIPLGNT 120
DB 61 GATFKALEOPHEISQRTTIVIOKQTFISQHSQVNSTELDELIOQIVAINAGIIPLGNT 120
QY 121 SNOISHWDLGSSFFPAGVITTTIGFNGISPRTEGKIFCIITIALGIFLPGFLLAGVGDQ 180
DB 121 SNOISHWDLGSSFFPAGVITTTIGFNGISPRTEGKIFCIITIALGIFLPGFLLAGVGDQ 180
QY 181 LGTFGKGIKAKVEDFFIKMNSQTKIRIISTIFILFGCVLFAVLPALIPKHIEGMSALD 240
DB 181 LGTFGKGIKAKVEDFFIKMNSQTKIRIISTIFILFGCVLFAVLPALIPKHIEGMSALD 240
QY 241 AIYFVVTITLTIGFGDYVAGSDIEYLDFFKPVVWFILVGLAYFAAVALSMIGWLRLVIS 300
DB 241 AIYFVVTITLTIGFGDYVAGSDIEYLDFFKPVVWFILVGLAYFAAVALSMIGWLRLVIS 300
QY 301 KKTKEVEGFRAHAEMTANTATAEFKETRRLSVEIYDKFORATSIRKLSAELAGNHQ 360
DB 301 KKTKEVEGFRAHAEMTANTATAEFKETRRLSVEIYDKFORATSIRKLSAELAGNHQ 360
QY 361 ELTPCRRITLNVHLTSEEDVLPPLLKTESIYINGLTPHACGEIYAVIENIK 411
DB 361 ELTPCRRITLNVHLTSEEDVLPPLLKTESIYINGLTPHACGEIYAVIENIK 411

```

RESULT 6  
US-09-939-484-8  
; Sequence 8, Application US/09939484  
; Patent No. US20020032322A1  
; GENERAL INFORMATION:  
; APPLICANT: Duprat, Fabrice  
; APPLICANT: Lesage, Florian  
; APPLICANT: Lazdunski, Michel  
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
; FILE REFERENCE: 1201-CIP-1IV-00  
; CURRENT APPLICATION NUMBER: US/09/939,484  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 09/144,914  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 08/749,816  
; PRIOR FILING DATE: 1996-11-15  
; PRIOR APPLICATION NUMBER: 60/095,234  
; PRIOR FILING DATE: 1998-08-04

; PRIOR APPLICATION NUMBER: FR 96/01565  
 ; PRIOR FILING DATE: 1996-02-08  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patentln Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 370  
 ; TYPE: PRT  
 ; ORGANISM: Murine  
 ; FEATURE:  
 ; OTHER INFORMATION: TREK-1  
 US-09-939-484-8

Query Match 86.9%; Score 1824; DB 9; Length 370;  
 Best Local Similarity 96.5%; Pred. No. 1,8e-170;  
 Matches 355; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDPTINVMKKTIVSTIFLVVLYLII 60  
 DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDPTINVMKKTIVSTIFLVVLYLII 60  
 QY 61 GATVFKALBOPHEISQRTTIVIOKOTFISQHSQVNSTELDELICQIVAAINAGIIPLGNT 120  
 DB 61 GATVFKALBOPHEISQRTTIVIOKOTFISQHSQVNSTELDELICQIVAAINAGIIPLGNS 120  
 QY 121 SNOISHMDLGSFFPAGTIVTTTIGFNGISPRTEGKIFCIYVALLGIPLEGFLAGVGQ 180  
 DB 121 SNOVSHMDLGSFFPAGTIVTTTIGFNGISPRTEGKIFCIYVALLGIPLEGFLAGVGQ 180  
 QY 181 LGTIFGKIAKVEDTFIKMNVSTQKIRIISTIIIFILEGCVLPVALPAVIFKHIEGMSALD 240  
 DB 181 LGTIFGKIAKVEDTFIKMNVSTQKIRIISTIIIFILEGCVLPVALPAVIFKHIEGMSALD 240  
 QY 241 AIFVTVITLTITIGFDVAGSDIEYDFKPVVFWIIVGLAFAAVISMIGDMRLVYS 300  
 DB 241 AIFVTVITLTITIGFDVAGSDIEYDFKPVVFWIIVGLAFAAVISMIGDMRLVYS 300  
 QY 301 KKTKEEVEGFRAHAEMTAVTAEFKETRRLSVEIYDKFORATSIKRKLASALAGNHQ 360  
 DB 301 KKTKEEVEGFRAHAEMTAVTAEFKETRRLSVEIYDKFORATSIKRKLASALAGNHQ 360  
 QY 361 ELTPCRRRT 368  
 DB 361 ELTPCRRRT 368

RESULT 7  
 US-09-939-483-8  
 ; Sequence 8, Application US/09939483  
 ; Patent No. US20020094558A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Duprat, Fabrice  
 ; APPLICANT: Lesage, Florian  
 ; APPLICANT: Fink, Michel  
 ; APPLICANT: Lazdunski, Michel  
 ; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
 ; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
 ; FILE REFERENCE: 1201-CIP-DIV-2-00  
 ; CURRENT APPLICATION NUMBER: US/09/939,483  
 ; PRIOR FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: 09/144,914  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: 08/749,816  
 ; PRIOR FILING DATE: 1996-11-15  
 ; PRIOR APPLICATION NUMBER: 60/095,234  
 ; PRIOR FILING DATE: 1998-08-04  
 ; PRIOR APPLICATION NUMBER: FR 96/01565  
 ; PRIOR FILING DATE: 1996-02-08  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patentln Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 370  
 ; TYPE: PRT  
 ; ORGANISM: Murine

; FEATURE:  
 ; OTHER INFORMATION: TREK-1  
 US-09-939-483-8

Query Match 86.9%; Score 1824; DB 9; Length 370;  
 Best Local Similarity 96.5%; Pred. No. 1,8e-170;  
 Matches 355; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDPTINVMKKTIVSTIFLVVLYLII 60  
 DB 1 MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVESDPTINVMKKTIVSTIFLVVLYLII 60  
 QY 61 GATVFKALBOPHEISQRTTIVIOKOTFISQHSQVNSTELDELICQIVAAINAGIIPLGNT 120  
 DB 61 GATVFKALBOPHEISQRTTIVIOKOTFISQHSQVNSTELDELICQIVAAINAGIIPLGNS 120  
 QY 121 SNOISHMDLGSFFPAGTIVTTTIGFNGISPRTEGKIFCIYVALLGIPLEGFLAGVGQ 180  
 DB 121 SNOVSHMDLGSFFPAGTIVTTTIGFNGISPRTEGKIFCIYVALLGIPLEGFLAGVGQ 180  
 QY 181 LGTIFGKIAKVEDTFIKMNVSTQKIRIISTIIIFILEGCVLPVALPAVIFKHIEGMSALD 240  
 DB 181 LGTIFGKIAKVEDTFIKMNVSTQKIRIISTIIIFILEGCVLPVALPAVIFKHIEGMSALD 240  
 QY 241 AIFVTVITLTITIGFDVAGSDIEYDFKPVVFWIIVGLAFAAVISMIGDMRLVYS 300  
 DB 241 AIFVTVITLTITIGFDVAGSDIEYDFKPVVFWIIVGLAFAAVISMIGDMRLVYS 300  
 QY 301 KKTKEEVEGFRAHAEMTAVTAEFKETRRLSVEIYDKFORATSIKRKLASALAGNHQ 360  
 DB 301 KKTKEEVEGFRAHAEMTAVTAEFKETRRLSVEIYDKFORATSIKRKLASALAGNHQ 360  
 QY 361 ELTPCRRRT 368  
 DB 361 ELTPCRRRT 368

RESULT 8  
 US-09-729-920-5  
 ; Sequence 5, Application US/09729920  
 ; Patent No. US20020103115A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GUEGLER, Karl et al  
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
 ; TITLE OF INVENTION: AND USNS THEREOF  
 ; FILE REFERENCE: C1000858  
 ; CURRENT APPLICATION NUMBER: US/09/729,920  
 ; PRIOR FILING DATE: 2000-12-06  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 538  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-09-729-920-5

Query Match 59.5%; Score 1248.5; DB 9; Length 538;  
 Best Local Similarity 64.6%; Pred. No. 1,2e-113;  
 Matches 244; Conservative 58; Mismatches 65; Indels 11; Gaps 5;

QY 2 MAAPDLDPKSA--AQNPKRLSFTKPTVLASRVESDT--TINVMKKTIVSTIFLVVLYLII 56  
 DB 23 MAAPVCPKSGATNGHHPVLPSTISSRATVVA--RMGASOGGIGQTVKMKKTIVVAIFVVVVV 81  
 QY 57 YLIIGATVPKALBOPHEISQRTTIVIOKOTFISQHSQVNSTELDELICQIVAAINAGIIP 116  
 DB 82 YLVATGIVFPAALBOPHEISQRTTIVIOKOTFISQHSQVNSTELDELICQIVAAINAGIIP 141  
 QY 117 LGTNSNQISHMDLGSFFPAGTIVTTTIGFNGISPRTEGKIFCIYVALLGIPLEGFLAG 176  
 DB 142 VGNSSNSSSHMDLGSFAFFAGTIVTTTIGYGNIAIPSTEGKIFCIYVALLGIPLEGFLAG 201



Query Match 59.2%; Score 1242.5; DB 9; Length 543;  
 Best Local Similarity 63.5%; Pred. No. 4.8e-113;  
 Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 2 AADPLDPKSA-----AONSKPRISFSTKPTVLASRVESDT--TINWKKMTVSTI 50  
 DB 22 AAAPVCCPKSATNGQPAPAPPTPTPLRLISSRATVVA-RMEGTSQGLQTVMKMTVVAI 80  
 QY FLVVVYLLIIGATVFKLEQPHIESORTTIVIOKQTFISQHSQVNSTEIDELIQOVAI 110  
 DB 81 FVVVVVLTGVLFRLEQPFESSQCNITALEKAEFLDHCVCVSQBLETLIQHALDD 140  
 QY 111 NAGIIPLGNTSNOISHNDLSSFFFAAGTVTTTIGFNGNISPRTEGKIFCIYVALLGIPLF 170  
 DB 141 NAGVSPFGNSNNSSHNDLSSAFFFAAGTVTTTIGYGNIAFSTEGKIFCIYVALLGIPLF 200  
 QY 171 GELLAGVDOLGTFPGSIGAKVEDTFTKMWVSOQTKRIRIITIFILFGCVLPALPAIF 230  
 DB 201 GFLLAGIGDGLTFPGSIRAKVEKVRKKQVSOQTKRIVSTILFILAGCIVFTVPAVIF 260  
 QY 231 KHIEGMSALDAIFYVYVITLTITIGFGDYVAGG-SDIEYLDIFYKVVWFWILVGLAYFAVYL 289  
 DB 261 KYIEGWTALBSIFVYVYVLTITVGFDPFVAGNGNAGIYREMYKPLVWFILVGLAYFAVYL 320  
 QY 290 SMIGDWLRVYSKTKKEVGEFRHAAAEWNTANTAEKTEFRRRLSVETIYKFGQATSI--- 346  
 DB 321 SMIGDWLRVYSKTKKEVGEVGIKAAAEWNTANTAEFRRRLSVETIYKFGQATSI--- 380  
 QY 347 -KRLSAELAGNHNQETPCRTU 369  
 DB 381 ERRRLGIDQRAHSLDMLSPKRSV 404

RESULT 12  
 US-10-262-511-106  
 ; Sequence 106, Application US/10262511  
 ; Publication No. US20040038223A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Smithson, Glenda  
 ; APPLICANT: Mallet, Isabelle  
 ; APPLICANT: Peyman, John A.  
 ; APPLICANT: Kekuda, Ramesh  
 ; APPLICANT: Ut, Jingfang  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Guo, Xiaojie (Sasha)  
 ; APPLICANT: Patuturajan, Meera  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Edinger, Shalom R.  
 ; APPLICANT: Ellerman, Karen  
 ; APPLICANT: Malvankar, Uriel M.  
 ; APPLICANT: Ort, Tatiana  
 ; APPLICANT: Gortman, Linda  
 ; APPLICANT: Zernhusen, Bryan D.  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Zhong, Mei  
 ; APPLICANT: Catterton, Blina  
 ; APPLICANT: Ji, Weizhen  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Stone, David J.  
 ; APPLICANT: Pena, Carol E. A.  
 ; APPLICANT: Shenoy, Suresh G.  
 ; APPLICANT: Shimkets, Richard A.  
 ; APPLICANT: Rothenberg, Mark E.  
 ; APPLICANT: Leach, Martin D.  
 ; APPLICANT: Agee, Michele L.  
 ; APPLICANT: Bergins, Constance  
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 ; FILE REFERENCE: 21402-462C  
 ; CURRENT APPLICATION NUMBER: US/10262,511  
 ; CURRENT FILING DATE: 2003-05-28  
 ; PRIOR APPLICATION NUMBER: 60/326,483

;; PRIOR FILING DATE: 2001-10-02  
 ;; PRIOR APPLICATION NUMBER: 60/373,815  
 ;; PRIOR FILING DATE: 2002-04-19  
 ;; PRIOR APPLICATION NUMBER: 60/327,917  
 ;; PRIOR FILING DATE: 2001-10-09  
 ;; PRIOR APPLICATION NUMBER: 60/381,642  
 ;; PRIOR FILING DATE: 2002-05-17  
 ;; PRIOR APPLICATION NUMBER: 60/328,029  
 ;; PRIOR FILING DATE: 2002-10-09  
 ;; PRIOR APPLICATION NUMBER: 60/381,038  
 ;; PRIOR FILING DATE: 2002-05-16  
 ;; PRIOR APPLICATION NUMBER: 60/328,056  
 ;; PRIOR FILING DATE: 2001-10-09  
 ;; PRIOR APPLICATION NUMBER: 60/373,260  
 ;; PRIOR FILING DATE: 2002-04-17  
 ;; PRIOR APPLICATION NUMBER: 60/373,826  
 ;; PRIOR FILING DATE: 2002-04-19  
 ;; PRIOR APPLICATION NUMBER: 60/327,435  
 ;; PRIOR FILING DATE: 2001-10-05  
 ;; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ;; NUMBER OF SEQ ID NOS: 439  
 ;; SOFTWARE: Cursesqlist version 0.1  
 ;; SEQ ID NO 106  
 ;; LENGTH: 543  
 ;; TYPE: PRT  
 ;; ORGANISM: Homo sapiens  
 US-10-262-511-106

Query Match 59.2%; Score 1242.5; DB 12; Length 543;  
 Best Local Similarity 63.5%; Pred. No. 4.8e-113;  
 Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 2 AADPLDPKSA-----AONSKPRISFSTKPTVLASRVESDT--TINWKKMTVSTI 50  
 DB 22 AAAPVCCPKSATNGQPAPAPPTPTPLRLISSRATVVA-RMEGTSQGLQTVMKMTVVAI 80  
 QY FLVVVYLLIIGATVFKLEQPHIESORTTIVIOKQTFISQHSQVNSTEIDELIQOVAI 110  
 DB 81 FVVVVVLTGVLFRLEQPFESSQCNITALEKAEFLDHCVCVSQBLETLIQHALDD 140  
 QY 111 NAGIIPLGNTSNOISHNDLSSFFFAAGTVTTTIGFNGNISPRTEGKIFCIYVALLGIPLF 170  
 DB 141 NAGVSPFGNSNNSSHNDLSSAFFFAAGTVTTTIGYGNIAFSTEGKIFCIYVALLGIPLF 200  
 QY 171 GELLAGVDOLGTFPGSIGAKVEDTFTKMWVSOQTKRIRIITIFILFGCVLPALPAIF 230  
 DB 201 GFLLAGIGDGLTFPGSIRAKVEKVRKKQVSOQTKRIVSTILFILAGCIVFTVPAVIF 260  
 QY 231 KHIEGMSALDAIFYVYVITLTITIGFGDYVAGG-SDIEYLDIFYKVVWFWILVGLAYFAVYL 289  
 DB 261 KYIEGWTALBSIFVYVYVLTITVGFDPFVAGNGNAGIYREMYKPLVWFILVGLAYFAVYL 320  
 QY 290 SMIGDWLRVYSKTKKEVGEFRHAAAEWNTANTAEKTEFRRRLSVETIYKFGQATSI--- 346  
 DB 321 SMIGDWLRVYSKTKKEVGEVGIKAAAEWNTANTAEFRRRLSVETIYKFGQATSI--- 380  
 QY 347 -KRLSAELAGNHNQETPCRTU 369  
 DB 381 ERRRLGIDQRAHSLDMLSPKRSV 404

RESULT 13  
 US-09-852-386-73  
 ; Sequence 73, Application US/09852386  
 ; Publication No. US20030064433A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Roderick, Steven L.  
 ; APPLICANT: Benjamin, Christopher  
 ; APPLICANT: Karnovsky, Chita M.  
 ; APPLICANT: Ruble, Cara L.  
 ; TITLE OF INVENTION: Human Ion Channels  
 ; FILE REFERENCE: 00133 US1  
 ; CURRENT APPLICATION NUMBER: US/09/852,386

```
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,305
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 60/207,092
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/206,526
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,033
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,093
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/216,893
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/237,873
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 60/223,245
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-386-73
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Query Match      59.2%; Score 1242.5; DB 12; Length 543;
Best Local Similarity 63.5%; Pred. No. 4.8e-113;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;
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QY 51 FLVVVLIIATVFKALQEPHEISORTTIVIOKOTFISCHSCVNSTELDELIQOIYAAI 110
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Db 81 FVVVVVIVTGVFRLAEQPFESSQKNTIALKAEFLRPHVCVSPQELTILIGHALDAD 140
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QY 111 NAGIIPLGNTSNQISHWDLGSSFFPAGTIVTTTIGFNGISPRTEGKIFCIYALGIPLF 170
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Db 141 NAGVSPIGNSSNNSSHMDLGSAPFFAGTIVTTTIGYGNAPSTEGKIFCIYALGIPLF 200
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QY 171 GFLLAGVDGLGTGFGKIAKVEDPTIKMNVSTQKIRIISTITILFGCVLFVALPAIIF 230
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Db 201 GFLLAGVDGLGTGFGKISIAVEKVPKQVSTQKIRIISTITILFGCVLFVALPAIIF 260
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QY 231 KHIEGMSALDAIYFVVVITLTITIGFDYVAGG-SDIEYLDYKPVWFWIIVGLAYFAAVL 289
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Db 261 KYIEGWTALSIYFVVVITLTITIGFDYVAGGSDIENYREMYKPLWFWIIVGLAYFAAVL 320
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Db 381 ERRRLGIDQRAHSLDMLSPKRSV 404
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RESULT 14
US-10-332-175-2
; Sequence 2, Application US/10332175
; Publication No. US20030176342A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. US20030176342A1el potassium channel
; FILE REFERENCE: Y0133PCT-666
; CURRENT APPLICATION NUMBER: US/10/332,175
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: JP 2000-396020
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 543
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-332-175-2
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Query Match      59.2%; Score 1242.5; DB 14; Length 543;
Best Local Similarity 63.5%; Pred. No. 4.8e-113;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;
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QY 51 FLVVVLIIATVFKALQEPHEISORTTIVIOKOTFISCHSCVNSTELDELIQOIYAAI 110
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Db 81 FVVVVVIVTGVFRLAEQPFESSQKNTIALKAEFLRPHVCVSPQELTILIGHALDAD 140
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 111 NAGIIPLGNTSNQISHWDLGSSFFPAGTIVTTTIGFNGISPRTEGKIFCIYALGIPLF 170
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 141 NAGVSPIGNSSNNSSHMDLGSAPFFAGTIVTTTIGYGNAPSTEGKIFCIYALGIPLF 200
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 171 GFLLAGVDGLGTGFGKIAKVEDPTIKMNVSTQKIRIISTITILFGCVLFVALPAIIF 230
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Db 201 GFLLAGVDGLGTGFGKISIAVEKVPKQVSTQKIRIISTITILFGCVLFVALPAIIF 260
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QY 231 KHIEGMSALDAIYFVVVITLTITIGFDYVAGG-SDIEYLDYKPVWFWIIVGLAYFAAVL 289
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 261 KYIEGWTALSIYFVVVITLTITIGFDYVAGGSDIENYREMYKPLWFWIIVGLAYFAAVL 320
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 290 SMIGDMWRVLSKTKKEVEGFRAHAAEWTAETVAPEFETRRRLSVEIYDKFORATSI--- 346
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 321 SMIGDMWRVLSKTKKEVEGEIKAHAAEWKANVTAPEFETRRRLSVEIHDKLOPAATIRSM 380
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 347 -KRKLAEIAGNHQELTPCRTL 369
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 381 ERRRLGIDQRAHSLDMLSPKRSV 404
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RESULT 15
US-10-332-447-10
; Sequence 10, Application US/10332447
; Publication No. US20040053258A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; RAUWANN, Brigitte E.;
; APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;
; APPLICANT: TANG, Y.Tom; HARLAND, Lee; BUREFORD, Neil;
; APPLICANT: GREENE, Barrie D.; SANTANVALA, Madhu S.;
; APPLICANT: BAUGHN, Mariah R.; YAO, Monique G.; YANG, Junming;
; APPLICANT: ARVIZU, Chandra S.; GANDHI, Ameena R.;
; APPLICANT: HAPFALIA, April J.A.; TRIBOULEY, Catherine M.;
; APPLICANT: WALIA, Nandinder K.; AU-YOUNG, Janice;
; APPLICANT: WALSH, Roderick T.; RAMKOVAR, Jayalakami;
; APPLICANT: LU, Yan; LU, Dying Aina M.; AZIMZAI, Yalda;
; APPLICANT: LAU, Preeti; ELLIOTT, Vicki S.; NGUYEN, Daniel B.;
; APPLICANT: XU, Yunting; SEILHAMER, Jeffrey J.; BOROMSKY, Mark L.;
; APPLICANT: KHAN, Farrah A.; KEARNEY, Liam; THANAVAVLU, Kavitha;
; APPLICANT: DAS, Debopriya; POLICKY, Jennifer L.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0149 USN
; CURRENT APPLICATION NUMBER: US/10/332,447
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/216,547
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/216,232
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/220,112
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/221,839
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 724
; TYPE: PRT
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ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20040053258A1 7472728CD1  
US-10-332-447-10

Query Match 57.9%; Score 1215; DB 12; Length 724;  
Best Local Similarity 62.1%; Pred. No. 3,7e-110;  
Matches 241; Conservative 58; Mismatches 67; Indels 22; Gaps 6;

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QY 2 AAPDLDPKSA-----AONSKPRLSESTKPTVLASRYESPT--TINMKMKTVSTI 50
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QY 51 FLVVVLYLIGATVFKALAEQPHIEISORTIVIOQTFIQHSQVNSTEIDELIQIVAAI 110
Db 259 FVVVVVYLVGTGVLFRALAEQPFESSQNTIALAKAEFLRDHVCVSPQELETLIQHALDAD 318
QY 111 NAGIIPLGNTSNQISHMDLGSFFFAQTVITTTIGFNGNISPRTEGKIFCIIVALLGIPLF 170
Db 319 NAGVSPIGNSSNNSSHMDLGSFAFFPAQTVITTM-YGNIAPEGKIFCIIVAFGIPLF 377
QY 171 GFLLAGVGDLGTIFGKIAKVEDTEIKMNVQSOTKIRIISTIIFFILFGCVLPAALPAIF 230
Db 378 GFLLAGIGDQLGTIFPKSIARVEKVRKQVSQTKIRISTILFIAGCIVFVTLPAVLF 437
QY 231 KHIEGWSALDAIFYVVYITLTITIGFDYVA---GGSDEYLDIFYKPVVWFMLVGLAYF 285
Db 438 KYIEGWTALESIYFVVYITLTITVGFDFVAVVFRGNAGINRYREWKPLVFWILVGLAYF 497
QY 286 AAVLSMTGMDLRYISKKEEVEGEFRRAAEWTANTAFKETRRLSVEIYDKFORATS 345
Db 498 AAVLSMTGMDLRYLSKKEEVEGEIKAAHAEMKANTAFRETRRLSVEIHDKFORAT 557
QY 346 I---KRLSAELAGNNOELTPCRRTL 369
Db 558 TRSMERRRLGLDQRAHSLDMLSPKRSV 585
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Search completed: July 15, 2004, 18:02:01  
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